

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Run on: April 27, 2003, 16:51:16 ; Search time 9337 Seconds

Title: US-09-787-657-3

sequence: 1 tactataggcgccgcgaa.....aaaaaaaaaaaaaaaa 3770

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:	Minimum match	0%
	Maximum match	100%

Listing first 45 summaries

Database :

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 41: em_hgo_other:*

Pred. No. is the number of results predicted by chance to have a

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3	3604.8	95.6	3690	6	AX427031	AX427031	Sequence
4	3394.2	90.0	3544	9	HSa27268	AX27268	Homo sapi
5	3329.6	87.2	3464	9	HSa272213	AX272213	Homo sapi
6	3229.6	85.7	3276	6	AX427033	AX427033	Sequence
7	3166.6	84.0	3213	6	AX098884	AX098884	Sequence
8	3166.0	84.0	3213	6	AX099304	AX099304	Sequence
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10	3113.6	82.6	3114	6	AX099303	AX099303	Sequence
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13	2956.6	78.4	3710	10	MMU010949	MMU010949	Mus muscu
14	1211.6	32.1	3209	6	AX098826	AX098926	Sequence
15	1211.6	32.1	3209	6	AX099346	AX099346	Sequence
16	1197.4	31.8	3339	6	AX098927	AX098927	Sequence
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18	1139.6	30.2	3201	6	AX098925	AX098925	Sequence
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ALIGNMENTS

RESULT	1
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LOCUS	AX098896
DEFINITION	Sequence 21 from Patent WO0119870.
ACCSSION	AX098896
VERSION	AX098896.1
KEYWORDS	GI:13538125
SOURCE	human.
ORGANISM	Homo sapiens
PAT	02-APR-2001
DNA	linear
bp	3770

REFERENCE
AUTHORS
TITLE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 3770)
Brown, J. P. and Bertelli, F.
Secreted soluble α (a) $_2$ -g(d)-2, -g(a) $_2$ -g(d)-3 or -g(a) $_2$ -g(d)-4
calcium channel subunit polypeptides and screening assays using

[illegible]

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AX099316			
LOCUS			
DEFINITION Sequence 21 from Patent WO0120336.			
ACCESSION AX099316			
VERSION AX099316.1 GI:13538471			
KEYWORDS			
SOURCE			
ORGANISM Homo sapiens			
human.			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
1 (bases 1 to 3770)			
Bertelli, F., Brown, J.P., Dissanayake, V., Suman-Chauhan, N. and			
Gee, N.S.			
Screening for alphasdelta-1 subunit binding ligands			
Patent: WO 0120336-A 21 22-MAR-2001;			
WARNER-LAMBERT COMPANY (US)			
FEATURES			
Source			
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Query Match 100.0%; Score 3769.6; DB 6; Length 3770;			

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RESULT 3
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LOCUS AX427031
DEFINITION Sequence 1 from Patent WO0194584.
ACCESSION AX427031
VERSION AX427031.1 GI:21530417
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Curtis, R.A.
TITLE 21784, a human calcium channel family member and uses thereof
JOURNAL Patent: WO 0194584-A 1 13-DEC-2001;
Milleinium Pharmaceuticals, Inc. (US)
FEATURES
source location/Qualifiers
1. 3690
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RESULT 4
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 LOCUS
 DEFINITION Homo sapiens mRNA for calcium channel alpha2-delta3 subunit.
 ACCESSION AJ272268
 VERSION AJ272268.1 GI:7105925
 KEYWORDS calcium channel alpha2-delta3 subunit.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 3544)
 Hanke,S., Bugert,P., Chudek,J. and Kovacs,G.
 Cloning a calcium channel alpha2delta3 subunit gene from a
 putative tumor suppressor gene region at chromosome 3p21.1 in
 conventional renal cell carcinoma
 Gene 264 (1), 69-75 (2001)
 JOURNAL
 MEDLINE 21142395
 PUBMED 11245980
 REFERENCE 2 (bases 1 to 3544)
 Kovacs,G.
 DIRECT SUBMISSION
 TITLE Direct Submission
 JOURNAL Submitted (15-FEB-2000) Kovacs G., Department of urology,
 University of Heidelberg, Laboratory of Molecular Oncology, Im
 Neuenheimer Feld 365, Heidelberg, 69120, GERMANY
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Oy	1978	TGGCGCTTTCAGAGGTTCATGGAATAATTTCTTCCGAGGGAATGTAAACCATGGAAGAAG	2037
Db	1783	TGGCGCTTTCAGAGGTTCATGGAATAATTTCTTCCGAGGGAATGTAAACCATGGAAGAAG	1842
Oy	2038	GCCATGATGACTTGAAGATCCGATGTGCTTGGCAGATGAATGGTCTTACTGCAACA	2097
Db	1843	GCCATGATGACTTGAAGATCCGATGTGCTTGGCAGATGAATGGTCTTACTGCAACA	1902
Oy	2098	CTGACCTACACCTTGAGCAGACCCGACTCTGCTCAGTTAGAGCGATTAGCTTACCTAA	2157
Db	1903	CTGACCTACACCTTGAGCAGACCCGACTCTGCTCAGTTAGAGCGATTAGCTTACCTAA	1962
Oy	2158	AAGGCAAGAACTCTGCTCCAGTGTGATAAAGATTGATCCAAAGAGTCCCTTTTGACG	2217
Db	1963	AAGGCAAGAACTCTGCTCCAGTGTGATAAAGATTGATCCAAAGAGTCCCTTTTGACG	2022
Oy	2218	CGGTGATGATGCCCCCAATTGAAGCGTATTGACACCGCTGGCCCTCAACAAATCTGAAA	2277
Db	2023	CGGTGATGATGCCCCCAATTGAAGCGTATTGACACCGCTGGCCCTCAACAAATCTGAAA	2082
Oy	2278	ATTCTGACAAAGGCGCTGAGAGTGTGCTTCTCGGCACTGCGACGGGCTCTCCAGAAATCA	2337
Db	2083	ATTCTGACAAAGGCGCTGAGAGTGTGCTTCTCGGCACTGCGACGGGCTCTCCAGAAATCA	2142
Oy	2338	ACCTGTTTGTGCGGGGCTGAGCAGCTCACCACATCAGAGCTTCCGAAAGTGGGCGCAAGG	2397
Db	2143	ACCTGTTTGTGCGGGGCTGAGCAGCTCACCACATCAGAGCTTCCGAAAGTGGGCGCAAGG	2202
Oy	2398	ACACATTTTAAACGAGACATTTCCCTCTGCTGATACGGAAGAGCCGCTGAGCAGATTTC	2457
Db	2203	ACACATTTTAAACGAGACATTTCCCTCTGCTGATACGGAAGAGCCGCTGAGCAGATTTC	2262
Oy	2458	CAGGGAGCTTGTCTACTGATGCCATTTAGCAGACTGACCACTCAATAAAGCAATGTGG	2517
Db	2263	CAGGGAGCTTGTCTACTGATGCCATTTAGCAGACTGACCACTCAATAAAGCAATGTGG	2322
Oy	2518	TGACAGCAAGTACATCCATCCAGCTCCCTGGATGAAGGAAATCTCCTGTGGGCGACGTG	2577
Db	2323	TGACAGCAAGTACATCCATCCAGCTCCCTGGATGAAGGAAATCTCCTGTGGGCGACGTG	2382
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Db	2383	TAGGCAATTCAGATGAAGAACTTGAATTTTCCAAAGAAAGTTCTGCACTGCGACAGACAGT	2442
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Db	2443	GTGCTTCCCTGGATGGCAATGCTCCATCAGCTGTGATGATGAGACTGTGAATTTGTACC	2502
Oy	2698	TCATAGCAATTAATGATTTATTTTGGTGTCTGAAGACTACACAGACTGAGACTTTT	2757
Db	2503	TCATAGCAATTAATGATTTATTTTGGTGTCTGAAGACTACACAGACTGAGACTTTT	2562
Oy	2758	TTGGTGAGATCGAGGAGCTGTGATGAACAAATTGCTTAACAATGGGCTCTTTAAAGAA	2817
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Db	2633	TTACCCCTTAAGACTACCAACCCATGTGTAGAGCCACAGAGAAAGCAGATGGCGCC	2682
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Db	2683	ATGGCCTTCTGATCTCTAATATGCTTCTCTGCGAGTAATAATGATTCATGACAGAAC	2742
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Db	2743	TTGCTCTGCTTCTGCTGGAATTTAACTCTGCAAGTTGGTGGCACTCCGATATGACAGCTA	2802
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Db	2803	AAGCCCAAAATTTGAAACAGACCTTGAGCCTTGTGATGATGAATATCCAGACTTGCTT	2862
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Oy	3298	TTCATCCTGAGAGAAATGCAAGGAGGTGGGGGTGGCGGAGTTCGCAAGCCAGACAG	3357
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Oy	3358	TCTCTCTTCTGCTCCCTCTGCTTTGATGCTCTTCAAGGTGACACTGAGATGTT	3417
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Oy	3718	GTGTACTTTTAAATTAAGTATATTAATCATTAATAAAAAAAAAAAAAAAAAA	3766
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LOCUS HSA272213
DEFINITION Homo sapiens mRNA for calcium channel alpha2-delta3 subunit (splice variant).
ACCESSION AJ272213
VERSION AJ272213.1 GI:7024360
KEYWORDS calcium channel alpha2-delta3 subunit.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3464)
AUTHORS Hanke,S., Bugert,P., Chudek,J., and Kovacs,G.
TITLE Cloning a calcium channel alpha2delta-3 subunit gene from a
putative tumor suppressor gene region at chromosome 3p21.1 in
conventional renal cell carcinoma
JOURNAL Gene 264 (1), 69-75 (2001)
MEDLINE 21142395
PUBMED 11245980
REFERENCE 2. (bases 1 to 3464)
AUTHORS Kovacs,G.

TITLE Direct Submission
JOURNAL Submitted (17-FEB-2000) Kovacs G., Department of Urology,
University of Heidelberg, Laboratory of Molecular Oncology, Im
Neuenheimer Feld 365, Heidelberg, 69120, GERMANY

FEATURES
Location/Qualifiers
1. 3464

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CDS

BASE COUNT 1003 a 762 c 834 g 865 t
ORIGIN

Query Match 87.2%; Score 3288.2; DB 9; Length 3464;
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Matches 3412; Conservative 1; Mismatches 9; Indels 89; Gaps 3;

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Db	1781	ATCCGATGTGTCCTTGGCAGATGAATGGTCTTACTCAACACAGTACCTACACCCCTAGC	1840
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QY	2176	TCCAGTGTGTTAAAGATGATCCAGAAATCCCTTTTGAACGGGTGTGTAAGTCCCCCA	2235
Db	1901	TCCAGTGTGTTAAAGATGATCCAGAAATCCCTTTTGAACGGGTGTGTAAGTCCCCCA	1960
QY	2236	TTGAACGATTTTGACACAGCCCTGGCCCTCAACAAATCTGAAATTTCTGAAAGGGCTGG	2295
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RESULT 6

AX427033

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

AX427033

Sequence 3 from Patent WO0194584.

AX427033

AX427033.1 GI:21530419

human.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

Curtis, R.A.

21784, a human calcium channel family member and uses thereof

Patent: WO 0194584-A 3 13-DEC-2001;

Millennium Pharmaceuticals, Inc. (US)

Location/Qualifiers

I. 3276

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Db	1501	GGCACAATGTGCCAGTGAAGAACTTCTGAAGACATCCCCAAATACAAATTAGGAGATT	1561
Oy	1686	CACGGTTATGCGTTTGGCAATCACAAATTAATGGRTATATCCGACGGATCCGGAACTCAGG	1741
Db	1561	CACGGTTATGCGTTTGGCAATCACAAATTAATGGRTATATCCGACGGATCCGGAACTCAGG	1621
Oy	1746	CTGCTGTACGAAAGAGGAAAAAAGCGAAGAAACCTAATATAGTACGTTGACCTCCT	1801
Db	1621	CTGCTGTACGAAAGAGGAAAAAAGCGAAGAAACCTAATATAGTACGTTGACCTCCT	1681
Oy	1806	GAGGTGCAATGGGAGACACCGAGATGACGTGTGGAAGATCTATGCTGAATCGAAAGACG	1861
Db	1681	GAGGTGCAATGGGAGAGACCGAGATGACGTGTGGAAGATCTATGCTGAATCGAAAGACG	1741
Oy	1866	GGGAAAGTTTTCCATGGAAGGTGAAGAAACACGTGGACAAAGGAAAGGGTTTTGGTGTATG	1921
Db	1741	GGGAAAGTTTTCCATGGAAGGTGAAGAAACACGTGGACAAAGGAAAGGGTTTTGGTGTATG	1801
Oy	1926	ACAAATGACTACTATTATACAGACATCAAGGGGTACTCCCTTCAAGTTAGGTGGGGGCTT	1981
Db	1801	ACAAATGACTACTATTATACAGACATCAAGGGGTACTCCCTTCAAGTTAGGTGGGGGCTT	1861
Oy	1986	TCCAGAGGTATCGGAAATATTTCTTCCGAGGGAATGTAAACATCGAAGAAAGGCTGTGAT	2041
Db	1861	TCCAGAGGTATCGGAAATATTTCTTCCGAGGGAATGTAAACATCGAAGAAAGGCTGTGAT	1921
Oy	2046	GACTTGAACATCCGATGTGTCTTGGCAGATGAATGGTCTTACTGCAACACTGACCTTA	2101
Db	1921	GACTTGAACATCCGATGTGTCTTGGCAGATGAATGGTCTTACTGCAACACTGACCTTA	1981
Oy	2106	CACCCGTAGACACCGGCATGTGTCTGATGATGAAGGATTAACCTGACTTAAGGCAAA	2161
Db	1981	CACCCGTAGACACCGGCATGTGTCTGATGATGAAGGATTAACCTGACTTAAGGCAAA	2041
Oy	2166	GAACCTTGTCTCAGTGTGATTAAGAAATGATCCAAAGATGCTTTTGTACGCGGTGGT	2221
Db	2041	GAACCTTGTCTCAGTGTGATTAAGAAATGATCCAAAGATGCTTTTGTACGCGGTGGT	2101

QY	2226	AGTGGCCCATTTGAAGCGTATGTGACACGCTTGCCCTCAACAATCTGAAATTTCTGAC	2285
Db	2101	AGTGGCCCATTTGAAGCGTATGTGACACGCTTGCCCTCAACAATCTGAAATTTCTGAC	2160
QY	2286	AAGGCGTGGAGGTTTGGCTTCTCTGGACACTGACACGGGCGTCCAGAAATCAACCTGTTT	2345
Db	2161	AAGGCGTGGAGGTTTGGCTTCTCTGGACACTGACACGGGCGTCCAGAAATCAACCTGTTT	2220
QY	2346	GTGCGGCGTGAAGCAGCTCACCAATCAGAGACTTCTTAAAGCTGGCAGCAAMGAGAACTT	2405
Db	2221	GTGCGGCGTGAAGCAGCTCACCAATCAGAGACTTCTTAAAGCTGGCAGCAAMGAGAACTT	2280
QY	2406	TTTAAACGACAGCAATTCCTCTCTCTGTGTACCGAAGAGCCGTGAGCAGATTCAGGAGGC	2465
Db	2281	TTTAAACGACAGCAATTCCTCTCTCTGTGTACCGAAGAGCCGTGAGCAGATTCAGGAGGC	2340
QY	2466	TTTCGCTCTCAGATCCCATTCCTCAGACAGCCAGCTCAATTTAAAGCAATGTGTGACACCA	2525
Db	2341	TTTCGCTCTCAGATCCCATTCCTCAGACAGCCAGCTCAATTTAAAGCAATGTGTGACACCA	2400
QY	2526	AGTACATCATCCAGCAGCTCTGAGATGAAGCAAGAAATTCCTGTGGTGGCAGCTGTAGACATT	2585
Db	2401	AGTACATCATCCAGCAGCTCTGAGATGAAGCAAGAAATTCCTGTGGTGGCAGCTGTAGACATT	2460
QY	2586	CAGATGAACCTTGAATTTTTCCAAAGAGATCTGAGACTGCCAGCAGACAGTGTCTTCC	2645
Db	2461	CAGATGAACCTTGAATTTTTCCAAAGAGATCTGAGACTGCCAGCAGACAGTGTCTTCC	2520
QY	2646	CTGGAATGGCAATCTCTCCATCAGCTGTGATGATGAACACTGTGAATTTGTTACTCTCAATAC	2705
Db	2521	CTGGAATGGCAATCTCTCCATCAGCTGTGATGATGAACACTGTGAATTTGTTACTCTCAATAC	2580
QY	2706	AATATGATTTATTTTGGTGTGGAAGATACACACAGCTGGAGACTTTTGTGGTAG	2765
Db	2581	AATATGATTTATTTTGGTGTGGAAGATACACACAGCTGGAGACTTTTGTGGTAG	2640
QY	2766	ATCGAGGAGCGCTGTGATGAACAATTTGCTAACATGGGCTCCTTTAAAGAAATTAACCTT	2825
Db	2641	ATCGAGGAGCGCTGTGATGAACAATTTGCTAACATGGGCTCCTTTAAAGAAATTAACCTT	2700
QY	2826	TATGACTAACCAAGCATGTGTAAAGCCACACAGAGAGAGCGGATGGCGCCCATGGCCTC	2885
Db	2701	TATGACTAACCAAGCATGTGTAAAGCCACACAGAGAGAGCGGATGGCGCCCATGGCCTC	2760
QY	2886	CTGATCCCTTATTAATGGCTTCCTCTCGCATGATGAATGGAATGATACAGAACTGTCTTG	2945
Db	2761	CTGATCCCTTATTAATGGCTTCCTCTCGCATGATGAATGGAATGATACAGAACTGTCTTG	2820
QY	2946	TTTCTGTGTGAATTTAACTCTGTGAGTTGGTGGCACTCCGATATGACAGTTAAAGCCAG	3005
Db	2821	TTTCTGTGTGAATTTAACTCTGTGAGTTGGTGGCACTCCGATATGACAGTTAAAGCCAG	2880
QY	3006	AAATTTGAACAGAGCCTTGAGGCTTGTATCTGAATATCCAGCAATTCGATCTGAGCGC	3065
Db	2881	AAATTTGAACAGAGCCTTGAGGCTTGTATCTGAATATCCAGCAATTCGATCTGAGCGC	2940
QY	3066	ACCATCAAGAGAGACTACAGGAATATTGTTGTGAAGACTGTCTCAAGTCTTTGTCTATC	3125
Db	2941	ACCATCAAGAGAGACTACAGGAATATTGTTGTGAAGACTGTCTCAAGTCTTTGTCTATC	3000
QY	3126	CAGCAAAATCCCAAGCAGCAACTGTCTCATGTGGTGGTGGAGCAGAGCTGACTCTGTGA	3185
Db	3001	CAGCAAAATCCCAAGCAGCAACTGTCTCATGTGGTGGTGGAGCAGAGCTGACTCTGTGA	3060
QY	3186	TTCTGTGCCCCCATCACCATGSCACCCATTTGAATCTAGTATTAATGAATTCCTTAAGTGT	3245
Db	3061	TTCTGTGCCCCCATCACCATGSCACCCATTTGAATCTAGTATTAATGAATTCCTTAAGTGT	3120
QY	3246	GAACGCTTAAAGGCCCAAGAGATCAGAAAGGCCCCAGAAATCTTGTCTATGTGCTTCATCT	3305
Db	3121	GAACGCTTAAAGGCCCAAGAGATCAGAAAGGCCCCAGAAATCTTGTCTATGTGCTTCATCT	3180

OY	3306	GAGAGAATGCAAGGGAGTGTGGGGSTGGCCGACAGTCCTCACAACCACAGACTCTCTTT	3365
Dd	3181		
OY	3366	CTGCCTCCCTCGCTTTTGATGCTCTCTCAAGGTGA	3401
Dd	3241		
Dd	3241	CTGCTCCCTCTGCTTTTGATGCTCTCTCAAGGTGA	3276
RESULT 7			
LOCUS	AX098884	3213 bp	DNA linear PAT 02-APR-2001
DEFINITION	Sequence 9 from Patent WO0119870.		
VERSION	AX098884		
KEYWORDS	AX098884.1 GI:13538120		
SOURCE	human.		
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 3213) Brown,J.P. and Bertelli,F. Secreted soluble _g(a)2,g(d)-2, _g(a)2,g(d)-3 or _g(a)2,g(d)-4 calcium channel subunit polypeptides and screening assays using same Patent: WO 0119870-A y 22-MAR-2001;		
JOURNAL	WARNER-LAMBERT COMPANY (US)		
FEATURES	Location/Qualifiers		
source	1..3213		
BASE COUNT	894 a 727 c 824 g 767 t 1 others		
ORIGIN			
Query Match	Best Local Similarity 84.0% Score 3166.6 DB 6 Length 3213:		
MATCHES	Matches 3195; Conservative 0; Mismatches 0; Indels 18; Gaps 1;		
OY	144	ATGGCGGGGCCGGGCTCGCGCGCGCGCGCGCTCCGGGGGGCCTCGGGCTTCGCTGCC	203
Dd	1	ATGGCGGGGCCGGGCTCGCGCGCGCGCGCGCTCCGGGGGGCCTCGGGCTTCGCTGCC	60
OY	204	GGGCTCTCTACGCGCGCGCTGGGGGACGTGCGCTCGACACAGATACCGCTCC	263
Dd	61	GGGCTCTCTACGCGCGCGCTGGGGGACGTGCGCTCGACACAGATACCGCTCC	120
OY	264	GTGTGAACCTCTGGGCTCGCGCTTTGGTGGGGAGATTAATTCATTGCTGTAAGTAC	323
Dd	121	GTGTGAACCTCTGGGCTCGCGCTTTGGTGGGGAGATTAATTCATTGCTGTAAGTAC	180
OY	324	TCCGGTCCACCTCTCGAAAAAATAACAAGATNAGAAAAGCTGGCCCATACAA	383
Dd	181	TCCGGTCCACCTCTCGAAAAAATAACAAGATNAGAAAAGCTGGCCCATACAA	240
OY	384	GAAATTTGATGGCTCCAACTGGTAAAGAGTGGCAAAGAACATGGAAGAGATTTTTAC	443
Dd	241	GAAATTTGATGGCTCCAACTGGTAAAGAGTGGCAAAGAACATGGAAGAGATTTTTAC	300
OY	444	AAGAAGCTGAGGCGCTGACGCGCTGGTGGAGSGCTGCAGAAAGCACACCTGAACAT	503
Dd	301	AAGAAGCTGAGGCGCTGACGCGCTGGTGGAGSGCTGCAGAAAGCACACCTGAACAT	360
OY	504	GAAATTTGATGAGCTTAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	563
Dd	361	GAAATTTGATGAGCTTAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	420
OY	564	AAAGACGGGAATTTTGGAGCTGGGAAAGAAATTCATTTAGCCCCAAATGACATTTT	623
Dd	421	AAAGACGGGAATTTTGGAGCTGGGAAAGAAATTCATTTAGCCCCAAATGACATTTT	480
OY	624	AATTAATTTGCTGTGACATCATGTCTAAGTACGTCCAAGTACCAAGACATGTACAC	683
Dd	481	AATTAATTTGCTGTGACATCATGTCTAAGTACGTCCAAGTACCAAGACATGTACAC	540

QY 684 AAAGACCTGCAATTTGCAATGGGTTTATTTGTTGATCTTAACAAGTTTTTTGTA 743
| | | | |
Db 541 AAAAGACCTGCAATTTGCAATGGGTTTATTTGTTGATCTTAACAAGTTTTTTGTA 600
| | | | |
QY 744 GATTAATTTGACCGTGAACCCATCTCTCATATGAGCAGTACTTTGGAGTGCAGAGGCTTT 803
| | | | |
Db 601 GATTAATTTGACCGTGAACCCATCTCTCATATGAGCAGTACTTTGGAGTGCAGAGGCTTT 660
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QY 804 TTTTGGAGATCCGGGGATTAATATGGGAACAGATAGAAATGGAGTCAATTTGCTTCGAC 863
| | | | |
Db 661 TTTTGGAGATCCGGGGATTAATATGGGAACAGATAGAAATGGAGTCAATTTGCTTCGAC 720
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QY 864 TGGAGAACCGAAATATGATACATCCAGCAGCAACTCTCCGAAAGAGGTCATTTTA 923
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Db 721 TGGAGAACCGAAATATGATACATCCAGCAGCAACTCTCCGAAAGAGGTCATTTTA 780
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QY 924 GTTGAAGTCAAGTGCAGCAGATGAAGAGACTCCGTCGATCTCGGAAGCAAGAGTCTCA 983
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Db 781 GTTGAAGTCAAGTGCAGCAGATGAAGAGACTCCGTCGATCTCGGAAGCAAGAGTCTCA 840
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QY 984 TCCATTTTGGATACATTTGGGGATGATGATCTTCAACATTAATTTGTTATATGAGAG 1043
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QY 1104 GAGCACTTGAAGGAGCATCTGACAAACTTTTGGCCAAAGAAATTTGGAATTTGATATA 1163
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QY 1164 GCTCTGAATGAGGCTTCAACATTTGATGATTTCAACACACCGGAGACAGAGATATC 1223
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Db 1021 GCTCTGAATGAGGCTTCAACATTTGATGATTTCAACACACCGGAGACAGAGATATC 1080
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QY 1224 TGCAGTCAGGCGCATCTGCTAATTAATGATGGGCGGTGAGACCTATGATCAATCTTT 1283
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Db 1081 TGCAGTCAGGCGCATCTGCTAATTAATGATGGGCGGTGAGACCTATGATCAATCTTT 1140
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QY 1284 GCAAAATACAAATTTGGCCAGATGGAAGGTTTGCATCTTACATACCTCAATTTGAGAGAG 1343
| | | | |
Db 1141 GCAAAATACAAATTTGGCCAGATGGAAGGTTTGCATCTTACATACCTCAATTTGAGAGAG 1200
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QY 1344 GCTGCTTGGCAGACAATCTAATGATGATGGGCTGTGCGCAACAAAGATTTTACCAG 1403
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QY 1404 ATCTCCACCTTGGCTGATGTGAGAGAGATGTATGAATACCTTCACGTGCTTACCGCG 1463
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QY 1584 CAGAACGAAACAGATGCAAGAGGCAATCTTCTGAGAGTGTGAGACAGATGTCCCACTG 1643
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QY 1704 ATCACAATATATGRTATATCTGAGCATCCGGAACCTCAGGCTGTGTACGAAGAAGA 1763
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QY 1764 AAAAAGCGAAGAAACCTTAATATATAGCGTTGACCTCTCTGAGGTGAGTGGAGAGAC 1823
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QY 1824 CGAGATGACGTTGAGAAATATGATGTAATGTAATGGAAGAGCGGAGAGTTTTCATGAG 1883
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QY 1884 GTGAAGAAGACAGTGAACAAAGGAAAGGTTTGTGATGACAAATGACTATTTAT 1943
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Db 1741 GTGAAGAAGACAGTGAACAAAGGAAAGGTTTGTGATGACAAATGACTATTTAT 1800
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QY 1944 ACAGACATCAAGGTAATCTCTTTCAGTTTATGATGAGGCTTTCCAGAGTCAATGGAAA 2003
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Db 1801 ACAGACATCAAGGTAATCTCTTTCAGTTTATGATGAGGCTTTCCAGAGTCAATGGAAA 1860
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QY 2004 TATTTCTCCGAGGAATGTAAACATGGAAGAGGCTGTGATGATTAAGATATCCCGAT 2063
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Db 1861 TATTTCTCCGAGGAATGTAAACATGGAAGAGGCTGTGATGATTAAGATATCCCGAT 1920
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QY 2064 GTGTCTTGGCAGATGAATGCTCTACTGCAACACTGACCTACACCTGAGCAGCCCAT 2123
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QY 2124 CTGTCTCAGTTAAGCGATTAAGCTCTTACCTTAAAGGCAAGAACCTTCTCAGTGT 2183
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Db 1981 CTGTCTCAGTTAAGCGATTAAGCTCTTACCTTAAAGGCAAGAACCTTCTCAGTGT 2040
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QY 2184 GATAAAGAAATTTGCAAGAGAGTCTTTTGAAGGCGGTGAGTGGCCCAATGGAAGG 2243
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QY 2244 TATTTGACAGGCTGCGCTCAACAAATCTGAAATTTGACAAAGGCGTGAAGTTGCC 2303
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Db 2161 TTTCTTGGCAGCTGCGCGGCTCTCAGAAATCAACTGTTTGTGCGGCTGAGCAGCTC 2220
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QY 2364 ACCAATCAGAGCTCTCTGAAAGCTGGCGCAGAGGAACATTTTAAAGCAACCATTTTC 2423
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Db 2221 ACCAATCAGAGCTCTCTGAAAGCTGGCGCAGAGGAACATTTTAAAGCAACCATTTTC 2280
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QY 2424 CCTCTCTGTGACGAAGAGCCGCTGAGCAGATTTCCAGGAGCTTGTCTACTGATCCCA 2483
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Db 2281 CCTCTCTGTGACGAAGAGCCGCTGAGCAGATTTCCAGGAGCTTGTCTACTGATCCCA 2340
| | | | |
QY 2484 TTTGACACTGAGCCAGTCAATTAAGCAATGTGTGAGACAGCAAGTACATCCAGCTC 2543
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Db 2341 TTTGACACTGAGCCAGTCAATTAAGCAATGTGTGAGACAGCAAGTACATCCAGCTC 2400
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QY 2544 CTGATGAAAGGAAATCTCTGTGTGAGAGCTGTAGGCAATTCAGATGAATCTGAATTT 2603
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Db 2401 CTGATGAAAGGAAATCTCTGTGTGAGAGCTGTAGGCAATTCAGATGAATCTGAATTT 2460
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QY 2604 TTTCCAAAGAAAGTTCTGAGCTGCCAGACAGAGTGTGCTTCCCTGATGAGCAAAATGCTCC 2663
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Db 2461 TTTCCAAAGAAAGTTCTGAGCTGCCAGACAGAGTGTGCTTCCCTGATGAGCAAAATGCTCC 2520
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QY 2724 GTGTCTGAAAGCTACACACAGACTGAGACTTTTGTGATGAGAGGAGCTGTATG 2783
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QY 2784 AACAATTTGCTAACAATGGGCTCTTTAAAGAAATTAACCTTTATGACTACCAAGCATG 2843
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QY 1704 ATCAACAATTAATGGTATATCTGAGGCAATCCGGAATCAGGCTGCTGTACGAAGAAGA 1763
Db 1561 ATCAACAATTAATGGTATATCTGAGGCAATCCGGAATCAGGCTGCTGTACGAAGAAGA 1620
QY 1764 AAAAAAGCAAGCAAACTAATATAGTAGGCTTACCTGCTGAGGTGAGAGTGGGAAGAC 1823
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Db 2161 TTCTCTGCACTGCGACGCGCTCTCCAGATCAACGTTTGTGCGGCTGAGCAGCTC 2220
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Db 2281 CCTCTCTGGATACGGAAGAGCGCGCTGACAGATTTCCAGGAGCTTCTGCTACTGATCCCA 2340

QY 2484 TTCAGCAGCTGGACCACTCAATTAAGCAATGTGTGACAGCAAGTACATCCAGCTC 2543
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Db 2401 CTGGATGACGGAATATCTCTGTGTGTGGGAGCTGTAGGCAATTCAGATGAACCTTGAATTT 2460
QY 2604 TTCAAAGAAATTTCTGACTGCGACAGACAGTGTGCTTCCCTGATGCAATGCTC 2663
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LOCUS 3114 bp DNA linear PART 02-Apr-2001
SEQUENCE 8 from Patent WO0119870.
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VERSION
KEYWORDS AX098883.1 GI:13538119
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 3114)
 AUTHORS Brown, J.P. and Bertelli, F.
 TITLE Secreted soluble -g(a)2-g(d)-2, -g(a)2-g(d)-3 cr -g(a)2-g(d)-4
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 JOURNAL Patent: WO 0119870-A 8 22-MAR-2001:
 WARNER-LAMBERT COMPANY (US)
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LOCUS AX099303
DEFINITION Sequence 8 from Patent WO0120336.
ACCESSION AX099303
VERSION AX099303.1 GI:13538465
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cranial; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3114)
AUTHORS Bertelli, F., Brown, J. P., Dissanayake, V., Suman-Chauhan, N. and
Ge, N. S.
TITLE Screening for alpha2delta-1 subunit binding ligands
JOURNAL Patent: WO 0120336-A 8 22-MAR-2001;
WARNER-LAMBERT COMPANY (US)
FEATURES
source location/Qualifiers
1. 3114
/organism="Homo sapiens"
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BASE COUNT 868 a 704 c 789 g 752 t 1 others
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS AX098882
DEFINITION Sequence 7 from Patent WO0119870.
ACCESSION AX098882
VERSION AX098882.1 GI:13538118
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Brown, J.P. and Bertelli, F.
TITLE Secreted soluble -g(a)2-g(d)-2, -g(a)2-g(d)-3 or -g(a)2-g(d)-4
calcium channel subunit polypeptides and screening assays using
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JOURNAL Patent: WO 0119870-A 7 22-MAR-2001;
WARNER-LAMBERT COMPANY (US)
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source 1. 3057
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Db 1201 GCTGCGTTTGCAGACAACTTAAGTGAATGAGCTGTGCAACAAAGAAATTTTATCCAG 1260
|||||
QY 1404 ATCTTCACCTTTGGCTGATGTGACAGAGAAATGTCAATGAAATACCTTCAAGCTT 1463
|||||
Db 1261 ATCTTCACCTTTGGCTGATGTGACAGAGAAATGTCAATGAAATACCTTCAAGCTT 1320
|||||
QY 1464 CCCAAAGTCAATGACACAGGAGCATGATGTGTGAGCGCAAGCTTCAATGACAGACT 1523
|||||
Db 1321 CCCAAAGTCAATGACACAGGAGCATGATGTGTGAGCGCAAGCTTCAATGACAGACT 1380
|||||

OY	1524	CGACGTATATCATCGGGCCCCGCTCTATATGACCACTGTAGCCATGCTGTGTTAGTAAG	1583
Db	1381	CTGTCTATATATCATCGGGCCCCGCTCTATATGACCACTGTAGCCATGCTGTGTTAGTAAG	1440
OY	1584	CAGAACCAAAACACATATGGAAGGGGCAATTCCTCTGGAGAGGGTGTGGCAGANGTCCCACTG	1643
Db	1441	CAGACGCAAAACCAATATGGAAGGGGCAATTCCTCTGGAGAGGGTGTGGCAGANGTCCCACTG	1500
OY	1644	AAGAAGCTTCTGAAGACCATCCCAAAATACAAATGTAGGGGATTCACGGTWTAGCTTTGCA	1703
Db	1501	AAGAAGCTTCTGAAGACCATCCCAAAATACAAATGTAGGGGATTCACGGTWTAGCTTTGCA	1560
OY	1704	ATCACAAATATATGTRTATATCTGTAGCCATTCGGAACTCAGGCTGTGTACGAAGAAGA	1763
Db	1561	ATCACAAATATATGTRTATATCTGTAGCCATTCGGAACTCAGGCTGTGTACGAAGAAGA	1620
OY	1764	AAAAAGGAAGGAACCTACTATATAGTAGGGTGAACCTCTCTGAGGTGAGTGGGAAGAC	1823
Db	1621	AAAAAGGAAGGAACCTACTATATAGTAGGGTGAACCTCTCTGAGGTGAGTGGGAAGAC	1680
OY	1824	CGAGATGACGCTGTTGGAAGATGCTATGTGAATCGAAGAAGCGGGAGAGTCTTCATGAG	1883
Db	1681	CGAGATGACGCTGTTGGAAGATGCTATGTGAATCGAAGAAGCGGGAGAGTCTTCATGAG	1740
OY	1884	GTAAGAAGACATGCAACAAGGGAACGGGCTTTGGTGATGACAAATGACTACTATTAT	1943
Db	1741	GTAAGAAGACATGCAACAAGGGAACGGGCTTTGGTGATGACAAATGACTACTATTAT	1800
OY	1944	ACAGACATCAAGGCTACTCTTCAAGTTAGTGGTGGCGCTTCCAGAGCTCATGGGAAA	2003
Db	1801	ACAGACATCAAGGCTACTCTTCAAGTTAGTGGTGGCGCTTCCAGAGCTCATGGGAAA	1860
OY	2004	TATTTCTTCCGAGGGAATGTAACCATCGAAGAAGCGCTGATACATAGAAACATCCCAT	2063
Db	1861	TATTTCTTCCGAGGGAATGTAACCATCGAAGAAGCGCTGATACATAGAAACATCCCAT	1920
OY	2064	GTGTCTTGTGGCAGATGAATGTGTCTTACTGCAACACTGACCTACCCCTGAGCAACCGCAT	2123
Db	1921	GTGTCTTGTGGCAGATGAATGTGTCTTACTGCAACACTGACCTACCCCTGAGCAACCGCAT	1980
OY	2124	GTGTCTCAATTTGAAGCGATTAAGCTCTACCTTAAAGGCAAGAACCTGTGCTCCAGTGT	2183
Db	1981	GTGTCTCAATTTGAAGCGATTAAGCTCTACCTTAAAGGCAAGAACCTGTGCTCCAGTGT	2040
OY	2184	GATTAAGAATGTATCCCAAAAGTCTCTTTTGACGCGGTGTGAGTGCCTCCCATTTGAAGG	2243
Db	2041	GATTAAGAATGTATCCCAAAAGTCTCTTTTGACGCGGTGTGAGTGCCTCCCATTTGAAGG	2100
OY	2244	TATTTGACCAAGCTTGCCCTCAACAACAAATCTGAAAAATTCTGACAAAGGCGCTGAGATTTGCC	2303
Db	2101	TATTTGACCAAGCTTGCCCTCAACAACAAATCTGAAAAATTCTGACAAAGGCGCTGAGATTTGCC	2160
OY	2304	TTTCCGCGGACCTGCGACGGGCGCTCTCCAGAAATCAACACTTTGTGTGGGGCTTGAGCAGCTC	2363
Db	2161	TTTCCGCGGACCTGCGACGGGCGCTCTCCAGAAATCAACACTTTGTGTGGGGCTTGAGCAGCTC	2220
OY	2364	ACCAATTCAGGACTTCTGAAAAGCTGGCGACAAGAGAACATTTTAAAGCCANACCAATTC	2423
Db	2221	ACCAATTCAGGACTTCTGAAAAGCTGGCGACAAGAGAACATTTTAAAGCCANACCAATTC	2280
OY	2424	CCTCTCTGTATCCGAAGAGCGCTGAGCAAGATTTCCAGGAGAGCTTGCTATATTCAGATCCA	2483
Db	2281	CCTCTCTGTATCCGAAGAGCGCTGAGCAAGATTTCCAGGAGAGCTTGCTATATTCAGATCCA	2340
OY	2484	TTTACACCTGGAGCGAGTAAATTAAGCAATGTGGTGAACAGCAAGTATCATCATCAAGCTC	2543
Db	2341	TTTACACCTGGAGCGAGTAAATTAAGCAATGTGGTGAACAGCAAGTATCATCATCAAGCTC	2400
OY	2544	CTGATGTAAGGAAATCTCTGTGTGTGACAGCTGTAGCAATTCAGATGAATCTGAATTT	2603
Db	2401	CTGATGTAAGGAAATCTCTGTGTGTGACAGCTGTAGCAATTCAGATGAATCTGAATTT	2460

[illegible]

QY 204 GCCTTCTCTACGCCGCTGGGGAGCTGCGCTCGGAGCAGATACCGCTGCC 263
| | | | |
Db 61 GCGCTTCTCTACGCCGCTGGGGAGCTGCGCTCGGAGCAGATACCGCTGCC 120
| | | | |
QY 264 GTGGTGAAGCTCTGGGCTTGGTGGGAGATAAATTCATGCTGCTAAGTAC 323
| | | | |
Db 121 GTGGTGAAGCTCTGGGCTTGGTGGGAGATAAATTCATGCTGCTAAGTAC 180
| | | | |
QY 324 TCGGTTCCGAGCTTCTGCAAAAAGATATGAGAAAGCCTTGGCATATGAA 383
| | | | |
Db 181 TCGGTTCCGAGCTTCTGCAAAAAGATATGAGAAAGCCTTGGCATATGAA 240
| | | | |
QY 384 GAAATTTGATGCGCTCCAACTGTAAAGAGCTGGCAAGAACTGAAAGATGTTTAC 443
| | | | |
Db 241 GAAATTTGATGCGCTCCAACTGTAAAGAGCTGGCAAGAACTGAAAGATGTTTAC 300
| | | | |
QY 444 AANAATCTGAGGCGCTCAGGCGCTCTGGTGGAGGCTGACAGAGAACACCTGAAACAT 503
| | | | |
Db 301 AANAATCTGAGGCGCTCAGGCGCTCTGGTGGAGGCTGACAGAGAACACCTGAAACAT 360
| | | | |
QY 504 GAATTTGATGCGAGCTTACAGTATGAAATCTTCAATGCTGCTGATTAATGAAAGGAC 563
| | | | |
Db 361 GAATTTGATGCGAGCTTACAGTATGAAATCTTCAATGCTGCTGATTAATGAAAGGAC 420
| | | | |
QY 564 AAGACGGGAATTTTGGAGCTGGGAAAGAAATTCATCTTACCCCAATGACATTTT 623
| | | | |
Db 421 AAGACGGGAATTTTGGAGCTGGGAAAGAAATTCATCTTACCCCAATGACATTTT 480
| | | | |
QY 624 AATTAATTTCCCTGTGAACATCACTTAAGTACGCTCCAAAGTACCAAGATGTACAC 683
| | | | |
Db 481 AATTAATTTCCCTGTGAACATCACTTAAGTACGCTCCAAAGTACCAAGATGTACAC 540
| | | | |
QY 684 AAGACCCCTGCAATTTCTCAATGGGGTTTATGGTCTGATCTCTAAACAAGCTTTTGA 743
| | | | |
Db 541 AAGACCCCTGCAATTTCTCAATGGGGTTTATGGTCTGATCTCTAAACAAGCTTTTGA 600
| | | | |
QY 744 GATTAATTTGACCGTGAACCATCTCTCATATGAGCACTTTGGAAGTCCAAAGGCTTT 803
| | | | |
Db 601 GATTAATTTGACCGTGAACCATCTCTCATATGAGCACTTTGGAAGTCCAAAGGCTTT 660
| | | | |
QY 804 TTTAGGCACTATCCGGGGTTTAAATGGGAAACGATGAGAAATGAGTCAATTCCTTGCAC 863
| | | | |
Db 661 TTTAGGCACTATCCGGGGTTTAAATGGGAAACGATGAGAAATGAGTCAATTCCTTGCAC 720
| | | | |
QY 864 TGCAGAACCCGAAATGTGATCATCCAGGAGCAGACCTTCCGAAAGACCTGCTCATTTTA 923
| | | | |
Db 721 TGCAGAACCCGAAATGTGATCATCCAGGAGCAGACCTTCCGAAAGACCTGCTCATTTTA 780
| | | | |
QY 924 GTTGACGTCACTGCGAGCATGAAAGAGCTCCGCTCTGACTATGCGAGCAACAGCTCTCA 983
| | | | |
Db 781 GTTGACGTCACTGCGAGCATGAAAGAGCTCCGCTCTGACTATGCGAGCAACAGCTCTCA 840
| | | | |
QY 984 TCCATTTTGGATACACTTGGGGATGATGACTTCTTCAACATTAATTTGCTTATTAAGAGAG 1043
| | | | |
Db 841 TCCATTTTGGATACACTTGGGGATGATGACTTCTTCAACATTAATTTGCTTATTAAGAGAG 900
| | | | |
QY 1044 CTTGACTATGTGAACCTTGGCTGAAATGGAATTTGGTGAACCCGAGAGCAACAAACA 1103
| | | | |
Db 901 CTTGACTATGTGAACCTTGGCTGAAATGGAATTTGGTGAACCCGAGAGCAACAAACA 960
| | | | |
QY 1104 GAGCAGCTTCAAGGAGCATCTGAGCAAACTTTTCCGCAAGAGAAATTTGGATATTA 1163
| | | | |
Db 961 GAGCAGCTTCAAGGAGCATCTGAGCAAACTTTTCCGCAAGAGAAATTTGGATATTA 1020
| | | | |
QY 1164 GCTTGTGAATGAGGCTTCAACATTTCTGAGTATTTCAACACAGCGGAGCAAGAGATATC 1223
| | | | |
Db 1021 GCTTGTGAATGAGGCTTCAACATTTCTGAGTATTTCAACACAGCGGAGCAAGAGATATC 1080
| | | | |
QY 1224 TGCAGTAGGCGCATGCTCATTAAGTATGAGGCGGTGGAGCACTATGATACATCTTT 1283
| | | | |
Db 1081 TGCAGTAGGCGCATGCTCATTAAGTATGAGGCGGTGGAGCACTATGATACATCTTT 1140
| | | | |
QY 1284 GCAAAATACAAATTTGCGAGATGCAAAAGTTTGCATCTTCACTACATCTTATTTGAGAGAG 1343
| | | | |

Db 1141 GCAAAATACAAATTTGCGAGATGCAAAAGTTTGCATCTTCACTACATCTTATTTGAGAGAG 1200
| | | | |
QY 1344 GCTGCGTTTCCAGCAATCTAAAGTGATGGCTGTGCTCCAAAGAGATTTTATACCAG 1403
| | | | |
Db 1201 GCTGCGTTTCCAGCAATCTAAAGTGATGGCTGTGCTCCAAAGAGATTTTATACCAG 1260
| | | | |
QY 1404 ATCTCCACTTGGCTGATGTGTGCAAGAGATGTATGGAATACCTTACGCTGTAGCCGG 1463
| | | | |
Db 1261 ATCTCCACTTGGCTGATGTGTGCAAGAGATGTATGGAATACCTTACGCTGTAGCCGG 1320
| | | | |
QY 1464 CCCAAGTCAATGCAAGAGAGCATGATGTGTGTGCAAGCAACCTTACATTTGACAGACT 1523
| | | | |
Db 1321 CCCAAGTCAATGCAAGAGAGCATGATGTGTGTGCAAGCAACCTTACATTTGACAGACT 1380
| | | | |
QY 1524 CTGACTGATGATCAGGCGCCGCTCTGATGACCACTGTATGCTGTGTTAGTAAG 1583
| | | | |
Db 1381 CTGACTGATGATCAGGCGCCGCTCTGATGACCACTGTATGCTGTGTTAGTAAG 1440
| | | | |
QY 1584 CAGAACGAAACCGATGCAAGGAGCTTCTTGGAGTGGTGGCAAGATGTCCAGTG 1643
| | | | |
Db 1441 CAGAACGAAACCGATGCAAGGAGCTTCTTGGAGTGGTGGCAAGATGTCCAGTG 1500
| | | | |
QY 1644 AAGACCTTCTGAGAGCAATCCCAATACAGTTAGGATTCACGCTTATGCTTTGCA 1703
| | | | |
Db 1501 AAGACCTTCTGAGAGCAATCCCAATACAGTTAGGATTCACGCTTATGCTTTGCA 1560
| | | | |
QY 1704 ATCCAAATTAATGATGATATCTGACGATCCGAGCACTAGGCTGCTGTACGAAAGAGA 1763
| | | | |
Db 1561 ATCCAAATTAATGATGATATCTGACGATCCGAGCACTAGGCTGCTGTACGAAAGAGA 1620
| | | | |
QY 1764 AAAAAAGGAAAGAACTTAATTAAGTACGCTGTGACCTCTGAGGTGAGTGGGAAGAC 1823
| | | | |
Db 1621 AAAAAAGGAAAGAACTTAATTAAGTACGCTGTGACCTCTGAGGTGAGTGGGAAGAC 1680
| | | | |
QY 1824 CGAGATGACGTGTGGAATGCTATGCTGATCCGAAAGCGGGGAATTTTCCATGAC 1883
| | | | |
Db 1681 CGAGATGACGTGTGGAATGCTATGCTGATCCGAAAGCGGGGAATTTTCCATGAC 1740
| | | | |
QY 1884 GTGAAGAGACAGTGGAGCAAAAGGAGGTTTGGTATGACAAATGATCACTATTAAT 1943
| | | | |
Db 1741 GTGAAGAGACAGTGGAGCAAAAGGAGGTTTGGTATGACAAATGATCACTATTAAT 1800
| | | | |
QY 1944 ACAGACATCAAGGATACCTCTTCAAGTTTAAAGTGGGCTTCCAGAGTCAATGGAAA 2003
| | | | |
Db 1801 ACAGACATCAAGGATACCTCTTCAAGTTTAAAGTGGGCTTCCAGAGTCAATGGAAA 1860
| | | | |
QY 2004 TATTTCTTCCGAGGGAATGTAAACCATGCAAGAGAGGCTGCACTTAAGAACATCCGAT 2063
| | | | |
Db 1861 TATTTCTTCCGAGGGAATGTAAACCATGCAAGAGAGGCTGCACTTAAGAACATCCGAT 1920
| | | | |
QY 2064 GTGTCCTTGGAGATGATGTGCTACTGCAACACTGACCTTACACCTCGAGACCGGCAT 2123
| | | | |
Db 1921 GTGTCCTTGGAGATGATGTGCTACTGCAACACTGACCTTACACCTCGAGACCGGCAT 1980
| | | | |
QY 2124 CTGTCTCAGTTAGAAAGCATTAAGCTTAACCTTAAAGGCAAAAGAACTCTCTCCAGTGT 2183
| | | | |
Db 1981 CTGTCTCAGTTAGAAAGCATTAAGCTTAACCTTAAAGGCAAAAGAACTCTCTCCAGTGT 2040
| | | | |
QY 2184 GATTAAGAAATTTGATCCAAAGAGCTTTTAAAGCGGTGTGAGTGTGCCCATTTGAAGCG 2243
| | | | |
Db 2041 GATTAAGAAATTTGATCCAAAGAGCTTTTAAAGCGGTGTGAGTGTGCCCATTTGAAGCG 2100
| | | | |
QY 2244 TATTTGACACAGCTTGGCCCTTCAACAAATCTGAAATTTCTGCAAGGCGGTGGAGCTTGGC 2303
| | | | |
Db 2101 TATTTGACACAGCTTGGCCCTTCAACAAATCTGAAATTTCTGCAAGGCGGTGGAGCTTGGC 2160
| | | | |
QY 2304 TTTCTGCGCACTGCGACGGGCTTCTCAGATCAACCTGTTTGTGGGGCTGAGACACTC 2363
| | | | |
Db 2161 TTTCTGCGCACTGCGACGGGCTTCTCAGATCAACCTGTTTGTGGGGCTGAGACACTC 2220
| | | | |
QY 2364 ACCAATGAGAGCTTCTGAAAGCTGGGAGACAGAGAACTTTTAAAGCAAGACATTTTC 2423
| | | | |

517 ACTTACAGTATGAATACCTCAATGCTGCTGATTAATGAAGGAGCAACAGCGGAATT 576
471 ACTTGACGTATGATTAATCTCAATCTGCTGATCAACAGAGGAGCAACAGCGGAATT 530
577 TTTTGGAGCTGGGAAGGAATTCATCTTAAAGCCCAATGACCAATTTTAAATTTGGCTG 636
531 TTTTGGAAATTTGGGAAGGAATTCATCTTAAAGCCCAATGACCAATTTTAAATTTGGCTG 590
637 TGAACATCAGTATGATGAGTCCCAATGACCAATGATGACCAATGATGACCAATGATGAC 696
591 TGAACATCAGTATGATGAGTCCCAATGACCAATGATGACCAATGATGACCAATGATGAC 650
697 TTTGCAATGGGCTTTTAAATGCTGCAATCTTAAACAAAGTTTGTGATTAATCTTAAAC 756
651 TTTGCAATGGGCTTTTAAATGCTGCAATCTTAAACAAAGTTTGTGATTAATCTTAAAC 710
757 GTTACACCATCTGCAATATGAGCACTTTTGAAGTGCAGAGGCTTTTAAAGCAGATATC 816
711 GGGATCCGCTCTCATATGAGCAGTACTTTGGAAGTGCAGAGGCTTTTAAAGCAGATATC 770
817 CGGGGATTTAAATGGGAACGATGAGAAATGAGATGATGCTTTCGACTGACAGACCGAA 876
771 CAGGATTTAAATGGGAACGATGAGAAATGAGATGATGCTTTCGACTGACAGACCGAA 830
877 AATGATACATCCAGGAGCAACTTCCGAAAGACGCTGCTTAAATGATGATGATGATGATG 936
831 AATGATACATCCAGGAGCAACTTCCGAAAGACGCTGCTTAAATGATGATGATGATGATG 890
937 GCAGCATGGAAGGACCTCCCTGCTGATGATGATGATGATGATGATGATGATGATGATG 996
891 GGAGCATGGAAGGACCTCCCTGCTGATGATGATGATGATGATGATGATGATGATGATG 950
997 CACTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1056
951 CTTGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1010
1057 AACCTTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1116
1011 AACCTTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1070
1117 AGCATCTGACAAACTTTTGGCCAAAGGAATGGAATGTTGATATATGCTGATGATGATG 1176
1071 AGCATCTGACAAACTTTTGGCCAAAGGAATGGAATGTTGATATATGCTGATGATGATG 1130
1177 CCTTACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1236
1131 CCTTACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1190
1237 TCATGCTCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1296
1191 TCATGCTCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1250
1297 GGGCAGATGCAAGAGTGGCATCTTACATACCTTATGATGATGATGATGATGATGATGATG 1356
1251 GGGCAGATGCAAGAGTGGCATCTTACATACCTTATGATGATGATGATGATGATGATGATG 1310
1357 ACAATCTTAAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1416
1311 ACAATCTTAAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1370
1417 CTGATGTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1476
1371 CTGATGTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1430
1477 ACCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1522
1431 ACCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1490
1523 -----TCTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1578
1491T AAAAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1550

1579 GTAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1638
1551 GTAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1610
1639 CAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1698
1611 CAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1670
1699 TTTGCAATCAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1758
1671 TTTGCAATCAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1730
1759 AAGCAAAAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1818
1731 AAGCAAAAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1790
1819 AAGCAAAAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1878
1791 AAGCAAAAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1850
1879 TGGAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1938
1851 TGGAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1910
1939 ATTATACAGATCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1998
1911 ACTATACAGATCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1970
1999 GGAATATATTTCTTCCGAGGGAATGATGATGATGATGATGATGATGATGATGATGATGATG 2058
1971 GGAATATATTTCTTCCGAGGGAATGATGATGATGATGATGATGATGATGATGATGATGATG 2030
2059 CCGATGTCCTTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2118
2031 CCGATGTCCTTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2090
2119 GGCATCTATCTCAAGTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 2178
2091 GGCATCTATCTCAAGTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 2150
2179 AGTGTATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2238
2151 AGTGTATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2210
2239 AAGCATATGGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2298
2211 AAGCATATGGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2270
2299 TTTGCTTCTCGGCACTGCGACGCGCTCTCCAGATCAACCTGTTTTCGCGGCTGAGC 2358
2271 TTTGCTTCTCGGCACTGCGACGCGCTCTCCAGATCAACCTGTTTTCGCGGCTGAGC 2330
2359 AGCTCACCATCAGGACCTTCCGAAAGCTGGGCAACAGGAGCAATTTTAAACGAGACC 2418
2331 AGCTCACCATCAGGACCTTCCGAAAGCTGGGCAACAGGAGCAATTTTAAACGAGACC 2390
2419 ATTTCCTCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 2478
2391 ATTTCCTCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 2450
2479 TTTGCTTCTCGGCACTGCGACGCGCTCTCCAGATCAACCTGTTTTCGCGGCTGAGC 2538
2451 TTTGCTTCTCGGCACTGCGACGCGCTCTCCAGATCAACCTGTTTTCGCGGCTGAGC 2510
2539 AGCTCACCATCAGGACCTTCCGAAAGCTGGGCAACAGGAGCAATTTTAAACGAGACC 2598
2511 AGCTCACCATCAGGACCTTCCGAAAGCTGGGCAACAGGAGCAATTTTAAACGAGACC 2570
2599 AATTTTTCGAAGAGGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 2658
2571 AATTTTTCGAAGAGGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 2630
2659 GCTTCATCAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2718

Db	2631	GCCTCAATACGCTGGATGAGAGACGCTGAACTTTACCTTATATGACATATACGATTCA	26300
QY	2719	TTTTGGTGTGAAAGACTACACACAGCTGGAGACTTTTTTGTGAGATCGAGGAGCTG	2778
Db	2691	TTCTGGGTCTGGAAGCTACACACAGACTGGAGATTTTTTTGGTGGAGTGAAGAGCTG	2750
QY	2779	TGATGAACAAATTGCTAACATGGGCTCTTTAAAGAAATTACCTTTATGACTACAG	2838
Db	2751	TCATGAACAAAGTTGTATACAAATGGGCTCTTTAAAGAAATACCTTTATGACTACAG	2810
QY	2839	CCATGTGTAGAGCCACACAGAAAGCAGCATGGCGGCCATGGCTCTGTGATCCTTATA	2898
Db	2811	CCATGTGTATAGCCACACAGAGAGAGCTGACACTGCCCCATGGACTTGTGACCCCTATA	2870
QY	2899	ATGCCCTTCTCTCTGCGAGTAAAAATGGATTCATGACAGAACTGTCTTTCTGTGTGAAT	2958
Db	2871	AGGCTCTTCTCTCTGCGAGCAAGTGATATMGAGCAACTGTCTTCTGTGTGAGT	2930
QY	2959	TTTAACCTCTGCACTTGGTGGCACTCCGATATGACAGCTAAAGCCAGAAATTGAACAGA	3018
Db	2931	TTTAACCTGTGCACTTGGTGGCACTCCGACATGACAGCTAAAGCCAGAAACTGAACAGA	2990
QY	3019	CCCTGAGACCTTGTGATACGAAATATACACATTCGTCGTCGTGAGCGACATCAAGAGA	3078
Db	2991	CCCTGAGACCTTGTGATACTGAAATACCCACGCTTTGTTCTGAAAGCAGCAATCAAGAGA	3050
QY	3079	CTACAGGGAATATTTGCTTGTGGAAGACTGTCACAAAGTCTTTGTCATCCAGCAATCCCAA	3138
Db	3051	CCACAGGGAACATTTGCTTGTGGAAGACTGTCACAAAGTCTTCTGTCATCCAACCAATCCCGA	3110
QY	3139	GCAGCAACCTGTTCAATGCTGTGTGTGTGACAGCAGCTGCTGTGTGAATCTGTGGCCCCCA	3198
Db	3111	GTACCAATCTGTTCATGCTGTGTGTGTGTGAGTAGTGTCTGTGTAOTCTGTGGCTCTTA	3170
QY	3199	TCACCATGGCAACCATTTGAAATATAGATATTAATCCCTTAAGTGTGAACGCTTAAGG	3258
Db	3171	TTAACCATGGCAACCATTTGAAATATAGATATTAATCCCTTAAGTGTGAACGCTTTAAGG	3230
QY	3259	CCCAGAAAGATCAGAAAGAGCCGCCAGAAATCTGTATGAGCTTCCATCCCGAGAGAGATCCAA	3318
Db	3231	CTACAGAAAGATCAGAGAGAGCTCCAGAAATCTGTATGAGCTTCCATCCCGAGAGAGATCCAA	3290
QY	3319	GGGAGTGTGGGGGTGCGCCGAGTCTCCAAAGCCAGACAGTCTCTTCTGCTGCTGCTGCTG	3378
Db	3291	GAGAGTGTGGGGGTGCTGATGAGTCTTCAAGGCCAGCGGCTTGTGCTGCTGCTGCTGCTG	3350
QY	3379	TTTTGTGCTCTTCTCAAGCTGACACTGTGACTGAGATGTTCTCTTACTGAATGAGATGTTCT	3438
Db	3351	TTTTGTGCTCTCTCTCAAGCTGACACTTACT-----ATMGAGGATGTTCT	3393
QY	3439	TCCTTGGCATGC--TAAATATGATGATTAATCTGTGAACCAAAATATGCTGCAACTATAGAGA	3496
Db	3394	TTTTGGCATGCTATTAATATCATGATTAATCTGTGAACCAACTATGCTGCAACTATAGAGA	3453
QY	3497	CATGAATATAGTCCAAACATCAAGCATCTTCATCATGATTTTAAACGTGTGCTGATATTAAC	3556
Db	3454	CATTAAGCATAGCCAGCCAGCATCAGCATC--TCATGATTTTAAACGTGTGCTGATATTAAC	3510
QY	3557	TCTTAAAGATATGTTGACAAAAAGTTATCTATTCATCTTTTAACTTTGCCAGTCAACAA	3616
Db	3511	TCTTAAAGATATGTTGACAAAAAGTT--ATCTTTTAACTTTGCCAGTCAACAA	3563
QY	3617	TGTGATTTGGCAGCATGATTAATCACCCCTTCATCAGAAATGGGAGCCGCAATGCTGAGCAG	3676
Db	3564	TGTGATTTGGCAGCATG--ATCACCCCTTCATCAGAAATGGGAGCTGATCGGCTAGCAG	3620
QY	3677	TGTCCCTTCTGCTGAAACCTATTTGAACCAATTTAAACCTGTACTTTTAAATATTAAG	3736
Db	3621	TGT--CCTTCTGCTGAAACCAATTTGAACCAATTTAAACCTGTACTTTTAAATATTAAG	3679
QY	3737	TATATTTAAATCATTAACAAAAAATAAAAA 3767	

Query Match	Best Local Similarity	Matches 1932; Conservative	Score 32.1%;	Pred. No. 1.5e-244;	Mismatches 1069;	Indels 39;	Gaps 4;
DB	3680	TATATTAAATCATTA	AAAAAAAAAAAAAAAAAAAA	3710			
RESULT 14							
LOCUS	AX098926	3209 bp	DNA	linear	PAT 02-APR-2001		
DEFINITION	Sequence 51 from Patent WO0119870.						
ACCESSION	AX098926						
VERSION	AX098926.1	GI:13538143					
KEYWORDS							
SOURCE	human.						
ORGANISM	Homo sapiens						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.						
AUTHORS	1 (bases 1 to 3209)						
TITLE	Brown, J.P. and Bertelli, F.						
JOURNAL	Secreted soluble -g(a)2,g(d)-2, -g(a)2,g(d)-3 or -g(a)2,g(d)-4 calcium channel subunit polypeptides and screening assays using same						
FEATURES	Patent: WO 0119870-A 51 22-MAR-2001; WARNER-LAMBERT COMPANY (US)						
source	Location/Qualifiers						
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OY	2041	TGCATGACTTAAAGACATCCCGATGTGTCTTTGGCAGATGAATGGTCTACTGCAACTG	2100
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GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: April 27, 2003, 20:10:56 ; Search time 4606 Seconds
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Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32:08132

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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DEFINITION 603027515F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5198015 5', mRNA sequence.

ACCESSION BI753834

VERSION BI753834.1 GI:15745412

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LAM1495 row: n column: 04

High quality sequence stop: 784.

Location/Qualifiers

1..966

SOURCE

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/clone_1lb="NIH_MGC_114"
/lab_host="DH10B"
/Note="Organ: brain; Vector: pCMV-Sport6; Site: 1: NotI; Site: 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH-MGC Library."
BASE COUNT      258 a      221 c      234 g      251 t      2 others
ORIGIN

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QY 3066 ACCATCAAGAGAGCTGTGAGAGAAATTTGCTGTGAGAGCTGTGAGAGCTGTGAGAGCT 3125
    |||||||
    541 ACCATCAAGAGAGCTGTGAGAGAAATTTGCTGTGAGAGCTGTGAGAGCTGTGAGAGCT 599
    |||||||

QY 3126 CAGCAAAATCCCAAGAGAGCAAACTGTTTCAATGATGATGATGATGATGATGATGATG 3185
    |||||||
    600 CAGCAAAATCCCAAGAGAGCAAACTGTTTCAATGATGATGATGATGATGATGATGATGATG 659
    |||||||

QY 3186 TCTGTGTGCCCCCATCAACATGACCCCATTTGAATTAATGATTAATGATTAATGATGAT 3245
    |||||||
    660 TCTGTGTGCCCCCATCAACATGACCCCATTTGAATTAATGATTAATGATTAATGATGAT 719
    |||||||

QY 3246 GAACTCTTAAGAGCCAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3305
    |||||||
    720 GAACTCTTAAGAGCCAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 776
    |||||||

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QY 3306 GAGGAGAAATGCAAGGAGAGTGTGGGGTGGCCGAGTCTCCAGCCAGAGAGTCTCTCT 3365
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    777 GAGGAGAAATGCAAGGAGAGTGTGGGGTGGCCGAGAGTCTCC-AGCCAGAGAGTCTCTCT 835
    |||||||

QY 3366 CTGTCGCCCTCTGCTTTTGAATGCTCTTCAAGGTACAGTACAGTACAGTGTCTTACT 3425
    |||||||
    836 TCTGTCCCTCTG-CTTTGATGCTCTTCTCAAGGTACAGTACAGTACAGTGTCTTACT 894
    |||||||

QY 3426 GACTGAGATGTTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3485
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    895 GACTGAGATGTT-TCCTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 951
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QY 3486 AATATACAGAGATG 3500
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    952 TACACACCTGAAATG 966
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RESULT 2
LOCUS      B1915864      880 bp      mRNA      linear      EST 16-Oct-2001
DEFINITION 603184526F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5248447 5',
            mRNA sequence.
ACCESSION  B1915864
VERSION    B1915864.1 GI:16179807
KEYWORDS   EST.
SOURCE      human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 880)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabs-remail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.lnl.gov
            Plate: LLM11627 row: c column: 08
            High quality sequence stop: 740.
            Location/Qualifiers
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                /db_xref="taxon:9606"
                /clone_1lb="NIH_MGC_121"
                /lab_host="DH10B"
                /Note="Organ: brain; Vector: pCMV-Sport6; Site: 1: NotI; Site: 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH-MGC Library."

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Query Match      20.8% Score 784.8; DB 13; Length 880;
Best Local Similarity 96.6%; Pred. No. 1.6e-125;
Matches 823; Conservative 0; Mismatches 27; Indels 2; Gaps 2;

QY 2921 ATGATCATGACAGAACTGTCTTCTGCTGAGAAATTAACCTGTGAGTGTGAGCA 2980
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    1 ATGATCATGACAGAACTGTCTTCTGCTGAGAAATTAACCTGTGAGTGTGAGCA 60
    |||||||

QY 2981 CTGCGATATGACAGCTTAAGCCCAAGAAATGAAACAGAGAGAGAGAGAGAGAGAGAG 3040
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Db	Accession	Gene	Species	Length
Db	61	CTCCGATATGACAGTAAAGCCAGAAATGAAACAGACCCCTGGAGCCCTGTGATATGTA		120
Qy	3041	ATATCCAGCATTCCTCTCTGTGAGCCGACCATCATCAAGAGACTACAGGAAATATTGCTTTGTA		3100
Db	121	ATATCCAGCATTCCTCTCTGTGAGCCGACCATCATCAAGAGACTACAGGAAATATTGCTTTGTA		180
Qy	3101	AGACTGCTCCAAAGTCTCTTGTGATCAGCAAAATCCCAAGCAGCAACCTTTCATGCTGT		3160
Db	181	AGACTGCTCCAAAGTCTCTTGTGATCAGCAAAATCCCAAGCAGCAACCTTTCATGCTGT		240
Qy	3161	GGTGACAGCAGCTGCTCTGTGAATCTGTGGCCCTCATCACATGAGCAACCATTTGAAT		3220
Db	241	GGTGACAGCAGCTGCTCTGTGAATCTGTGGCCCTCATCACATGAGCAACCATTTGAAT		300
Qy	3221	CAGGTATATGTAATCCCTTAAAGTGTGAACGCTCTAAAGGCCAGAAATACAGAGGCCGCC		3280
Db	301	CAGGTATATGTAATCCCTTAAAGTGTGAACGCTCTAAAGGCCAGAAATACAGAGGCCGCC		360
Qy	3281	AGAACTCTGTATGGCTTCCATCCCTGAGAGAAATCCAGAGGAGTGTGGGGGCGCCGAG		3340
Db	361	AGAACTCTGTATGGCTTCCATCCCTGAGAGAAATCCAGAGGAGTGTGGGGGCGCCGAG		420
Qy	3341	TCTCCAAAGCCAGCAGCTGCTCTGTGATCAGCAAAATCCCAAGCAGCAACCTTTCATGCTGT		3399
Db	421	TCTCCAAAGCCAGCAGCTGCTCTGTGATCAGCAAAATCCCAAGCAGCAACCTTTCATGCTGT		480
Qy	3400	GACACTGACAGATGTTCTCTTACTGACATGATTTCTCTTGGCATCTTAAATCATAG		3459
Db	481	GACACTGACAGATGTTCTCTTACTGACATGATTTCTCTTGGCATCTTAAATCATAG		540
Qy	3460	ATTAACCTGTGAACCAAAATATGTGTCAACATTCAGACATGATATAGTCCACCATCAG		3519
Db	541	ATTAACCTGTGAACCAAAATATGTGTCAACATTCAGACATGATATAGTCCACCATCAG		600
Qy	3520	CATCTCATCATGATTTTAAACGTGCGATATTAACCTTAAAGATATGTTGACAAATA		3579
Db	601	CATCTCATCATGATTTTAAACGTGCGATATTAACCTTAAAGATATGTTGACAAATA		660
Qy	3580	GTTATCTCATCTTTTACTTTTGGCAGTCAATGCAAAATGTGATTTGGCAGTCAATCT		3639
Db	661	GTTATCTCATCTTTTACTTTTGGCAGTCAATGCAAAATGTGATTTGGCAGTCAATCT		720
Qy	3640	ACCCTTCATCAGAAATGGAGCCGACAGTGTGTA-GGACGTGTCCTTCTCTTGAACCTTA		3698
Db	721	ACCCTTCATCAGAAATGGAGCCGACAGTGTGTA-GGACGTGTCCTTCTCTTGAACCTTA		780
Qy	3699	TTGAAACCAATTTAAACTGTGTACTTTTAAATTAATTAATTAATTAATTAATTAATTAAT		3758
Db	781	ATCGAACCAATTTAAACTGTGTACTTTTAAATTAATTAATTAATTAATTAATTAATTAAT		840
Qy	3759	AAAAAAAAAAAAA 3770		
Db	841	AAAAAAAAAAAAA 852		

TITLE	Creation of genome-wide protein expression libraries using random
JOURNAL	activation of gene expression
MEDLINE	Nat. Biotechnol. 19 (5), 440-445 (2001)
COMMENT	21227151 Contact: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scaine@atersys.com High quality sequence stop: 551. Location/Qualifiers 1..798 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="Athersys RAGE library" /cell_line="HT1080" /note="See 'Creation of Genome-wide Protein Expression' Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
FEATURES	
source	
BASE COUNT	215 a 196 c 178 g 209 t
ORIGIN	
Query Match	20.8%; Score 784.2; DB 12; Length 798;
Best Local Similarity	99.0%; Pred. No. 2e-125;
Matches 789; Conservative 0; Mismatches 8; Indels 0; Gaps 0.	
QY 2822	CCTTTATGACTACCAAGCCATGTGTAGAGCCACAAGAAAGCAGGATGGGCCCATGG 2881
Db 1	CCTCATATCACTACCATGCGCATGTGTAGAGCCACAAGAAAGCAGGATGGGCCCATGG 60
QY 2882	CCTCTGGATCCTTATTAATGCTTCCTCTCTGACAGTAAATGAGATCACAAGAACTTGT 2941
Db 61	CCTCTGGATCCTTATTAATGCTTCCTCTCTGACAGTAAATGAGATCACAAGAACTTGT 120
QY 2942	CTTGTTCCTGTGGTAATTTAACTCTGCAGTTGTGTGGCACTCCGATATGACAGCTAAAGC 3001
Db 121	CTTGTTCCTGTGGTAATTTAACTCTGCAGTTGTGTGGCACTCCGATATGACAGCTAAAGC 180
QY 3002	CCAGAAATTTGAACAAGACCCCTGGAGCCTTGTGATCTGAATATCCAGATTCGTCTCTGA 3061
Db 181	CCAGAAATTTGAACAAGACCCCTGGAGCCTTGTGATCTGAATATCCAGATTCGTCTCTGA 240
QY 3062	GCGCAACCATCAAGAGAGACTACAGGGAATATTCCTTGTGAAGACTGCTCCAACTCTTGT 3121
Db 241	GCGCAACCATCAAGAGAGACTACAGGGAATATTCCTTGTGAAGACTGCTCCAACTCTTGT 300
QY 3122	CATCCAGCAAAATCCCAAGAGACCACTCTGTATGAGTGGGTGGAGACAGAGCTGCCTTG 3181
Db 301	CATCCAGCAAAATCCCAAGAGACCACTCTGTATGAGTGGGTGGAGACAGAGCTGCCTTG 360
QY 3182	TGAATCTGTGGCCCCCATATCACCATTGGCAACCCATTTGAATCAGATTAATGAATGCCCTTAA 3241
Db 361	TGAATCTGTGGCCCCCATATCACCATTGGCAACCCATTTGAATCAGATTAATGAATGCCCTTAA 420
QY 3242	GTTGTCAGCTCTAAAGGCCACAGAGATCAGAAGGCGCCAGATCTTGTTCATGTGCTTCCA 3301
Db 421	GTTGTCAGCTCTAAAGGCCACAGAGATCAGAAGGCGCCAGATCTTGTTCATGTGCTTCCA 480
QY 3302	TTCGAGAGAGAAATGCAAGGAGTGTGGGGGTGGCGAGTCTCCAAAGCCCAACAGAGTCT 3361
Db 481	TTCGAGAGAGAAATGCAAGGAGTGTGGGGGTGGCGAGTCTCCAAAGCCCAACAGAGTCT 540
QY 3362	CCTTCTGTCCCTCTGCTTTTGTGATCTCTTTCAGAGTGACACTACTAGATGATGTTCTCT 3421
Db 541	CCTTCTGTCCCTCTGCTTTTGTGATCTCTTTCAGAGTGACACTACTAGATGATGTTCTCT 600
QY 3422	TACTGACTGAGATGTTCTCTTGGCATGCTAAATCATGAGATAAATCTGTGAACCAAAATATG 3481
Db 601	TACTGACTGAGATGTTCTCTTGGCATGCTAAATCATGAGATAAATCTGTGAACCAAAATATG 660

OY	2312	CACATCGCAGGGGCTCTCCAGAAATCACACTGTTTTGTGCGGGGGTGAGAGCTGCACCAATCA	2371
Db	241	CACTCGACGGGCCCTCTCCAGAATCAACACTCTTTTGTGCGGGGGTGAGAGCTGCACCAATCA	300
OY	2372	GGAATCTCTGAAGAGCTGGGACAAGAGAAACATTTTTTAACGACAGACCATTTCCTCTGTG	2431
Db	301	GGACTTCTCTAAGAGCTGGGACAAGAGAACATTTTTTAACGACAGACCATTTCCTCTGTG	360
OY	2432	GTACCGAAGCCGCTGAGAGATTTCCAGGAGCTTCGTCTACTCGATCCCATTCAGCAC	2491
Db	361	GTACCGAAGCCGCTGAGAGATTTCCAGGAGCTTCGTCTACTCGATCCCATTCAGCAC	420
OY	2492	TGGACAGTCATAAAGCAATGTGGTGACAGCAAGTACATCCATCCAGTCCCTGGATGA	2551
Db	421	TGGACAGTCATAAAGCAATGTGGTGACAGCAAGTACATCCATCCAGTCCCTGGATGA	480
OY	2552	ACGGAATCTCTCTGTGGTGACAGCTGTAGGCATTCAGATGAACCTTGAATTTTTCCAAAG	2611
Db	481	ACGGAATCTCTCTGTGGTGACAGCTGTAGGCATTCAGATGAACCTTGAATTTTTCCAAAG	540
OY	2612	GAGTCTGTGAGCTGGCAGAGACAGTGTCTCTCCGATGSCAAATGCTCATCAGCTG	2671
Db	541	GATGTTCTGTGAGCTGGCAGAGACAGTGTCTCTCCGATGSCAAATGCTCATCAGCTG	600
OY	2672	TGATGATGAGAGCTGTGAATTTGTACCTCAATAGACATTAATGATTTAATTTGGTGCTGA	2731
Db	601	TGATGATGAGAGCTGTGAATTTGTACCTCAATAGACATTAATGATTTAATTTGGTGCTGA	659
OY	2732	AACACTACACACAGACTGGAGACTTTTTTGGTGAGATCGAGGAGCTGTGATGAACAAAT	2791
Db	660	AACACTACACACAGACTGGAGACTTTTTTGGTGAGATCGAGGAGCTGTGATGAACAAAT	715
OY	2792	GCTAACATGAGCTCTCTT 2809	
Db	716	GCTAACATGAGCTCTCTT 733	
RESULT 5			
LOCUS	BE740459	818 bp	mRNA linear EST 15-SEP-2000
DEFINITION	601595508B1 NIH_MGC_9 Homo sapiens CDNA clone IMAGE:3949657 5'		
ACCESSION	BE740459		
VERSION	BE740459.1 GI:10154451		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 818)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cga@rsf-mail.nih.gov Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: Image.llnl.gov Plate: LHCMB14 row: O column: 02 High quality sequence stop: 774. Location/Qualifiers 1. 818 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:3949657" /clone_lib="NIH_MGC_9" /tissue_type="adenocarcinoma cell line" /lab_host="DH10B (phage-resistant)" /note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:		

ECORI: cDNA made by oligo-dT priming. Directionally cloned into EcorI/XhoI sites using the following 5' adaptor: GGACGAG(g). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 244 a 169 c 205 g 200 t
 Query Match 17.2%; Score 647.2; DB 12; Length 818;
 Best Local Similarity 89.4%; Pred. No. 8.2e-102;
 Matches 794; Conservative 1; Mismatches 14; Indels 79; Gaps 6;

QY 954 CGTCTGACTATCGGGAACAACAGCTCCATTCATTTGGATACACTTGGGATGATGAC 1013
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 QY 1014 TTCTTCAACATTAATGCTTTATATGAGAGGCTTCACTATGTGAACTTGGCTGAATGA 1073
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 QY 1074 ACTTTGGTGAAGCCGACAGACAAACAAAGAGCCTTCAGGGAGCATTTGGACAACTT 1133
 DB 121 ACTTTGGTGAAGCCGACAGACAAACAAAGAGCCTTCAGGGAGCATTTGGACAACTT 180
 QY 1134 TTGCGCAAGAAATTTGGAATTTGGATATAGCTCTGATGATGAGGCTTCACATCTGAGT 1193
 DB 181 TTGCGCAAGAAATTTGGAATTTGGATATAGCTCTGATGATGAGGCTTCACATCTGAGT 240
 QY 1194 GATTTCACACACAGGACAAAGAAATTTGTCAGTCAGGCTCATGCTCATTAACATGAT 1253
 DB 241 GATTTCACACACAGGACAAAGAAATTTGTCAGTCAGGCTCATGCTCATTAACATGAT 300
 QY 1254 GGGGCGGTGACACCTTATGATATCAATCTTGGCAAAATGCAATGGCCAAATCGAAAGTT 1313
 DB 301 GGGGCGGTGACACCTTATGATATCAATCTTGGCAAAATGCAATGGCCAAATCGAAAGTT 360
 QY 1314 CGCATCTTCACATACCTTATGATGACGAGAGGCTGCGTTTCAGACAAATTTAAAGTGGATG 1373
 DB 361 CGCATCTTCACATACCTTATGATGACGAGAGGCTGCGTTTCAGACAAATTTAAAGTGGATG 420
 QY 1374 GCGTGTGCCAACAAGATTTTACCAGATCTCCACCTTGGCTGATTTGCAAGAGAAAT 1433
 DB 421 GCGTGTGCCAACAAGATTTTACCAGATCTCCACCTTGGCTGATTTGCAAGAGAAAT 480
 QY 1434 GTCATGGAATACCTTACAGGCTTAGCGGCGCAAAAGTCAATGACCAAGAGCATGATGTC 1493
 DB 481 GTCATGGAATACCTTACAGGCTTAGCGGCGCAAAAGTCAATGACCAAGAGCATGATGTC 539
 QY 1494 GTGTGACCAAGACCTTACATTTGACAGCAGCTCTGATGATGATCAGGGCCCGCTCTGATG 1553
 DB 540 GTGTGACCAAGACCTTACATTTGACAGCAGCTCTGATGATGATCAGGGCCCGCTCTGATG 569
 QY 1554 ACCACGTGAGCCATGCTGCTGTTTAAAGACAGCAACCAAGATCGAAGGCAATCTT 1613
 DB 570 ACCACGTGAGCCATGCTGCTGTTTAAAGACAGCAACCAAGATCGAAGGCAATCTT 587
 QY 1614 CTGGAGATGTTGGACAGATGTCAGTGAAGAAAGACTTCTGAAGACCTTCCCAAAATAC 1673
 DB 588 CTGGAGATGTTGGACAGATGTTCCAGTGAAGAAAGACTTCTGAAGAAATCCCAAAATAC 647
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 DB 707 CCGGAACCTGAGCTGCTGTACGAAGAAGAAAGCAAGAACTTACTATGATGAC 762
 QY 1794 GTTGAACCTTCTGAGGTGAGTGGAGCAAGACGATGATGATGATGATGATGATGATGATGAT 1841
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RESULT 6
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 LOCUS
 DEFINITION
 RST33037 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
 BG213431
 VERSION
 BG213431.1 GI:13735118
 KEYWORDS
 EST.

SOURCE
 human.

ORGANISM
 Homo sapiens

REFERENCE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 801)

AUTHORS
 Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
 Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J.,
 Leiner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,
 J., Danzig,J., and Ducar,M.
 Creation of genome-wide protein expression libraries using random
 activation of gene expression
 Nat. Biotechnol. 19 (5), 440-445 (2001)

TITLE
 JOURNAL
 MEDLINE
 21227151
 21227151

COMMENT
 Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scain@atersys.com
 High quality sequence stop: 477.
 location/qualifiers
 1. 801

FEATURES
 source
 1. 801
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Athersys RAGE Library"
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 /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 221 a 191 c 183 g 205 t 1 others
 ORIGIN

Query Match 16.8%; Score 633.4; DB 12; Length 801;
 Best Local Similarity 91.3%; Pred. No. 2e-99;
 Matches 723; Conservative 0; Mismatches 22; Indels 47; Gaps 3;

QY 2688 AATTGTACTCATAGCAATTAATGATTTATTTGGTGTCTGAAGCTACACAGACT 2747
 DB 13 AATTGTACTCATAGCAATTAATGATTTATTTGGTGTCTGAAGCTACACAGACT 72
 QY 2748 GGAGACTTTTGGTGTGATCGAGGAGCTGTGATGAACAATTTGCTAATGAGGCTCC 2807
 DB 73 GGAGACTTTTGGTGTGATCGAGGAGCTGTGATGAACAATTTGCTAATGAGGCTCC 132
 QY 2808 TTTAAAAAATTAACCTTTATGACTACCAAGCCATGTGTAGAGCCAAAGAAAGCAGC 2867
 DB 133 TTTAAAAAATTAACCTTTATGACTACCAAGCCATGTGTAGAGCCAAAGAAAGCAGC 192
 QY 2868 GATGGGCCCATGGCCCTCCGATCCCTTAAATGAGCTTCTCTGAGTAAATGATGAT 2927
 DB 193 GATGGGCCCATGGCCCTCCGATCCCTTAAATGAGCTTCTCTGAGTAAATGATGAT 252
 QY 2928 ATGACAGAACTTGTCTTGTCTGCTGTGGAATTTAACTCTGAGTGTGTGCTCCGAT 2987
 DB 253 ATGACAGAACTTGTCTTGTCTGCTGTGGAATTTAACTCTGAGTGTGTGCTCCGAT 312
 QY 2988 ATGACAGCTTAAAGCCAGAAATTTGAACAGACCTTGGAGCTTGTGATCTGATATCA 3047
 DB 313 ATGACAGCTTAAAGCCAGAAATTTGAACAGACCTTGGAGCTTGTGATCTGATATCA 372

QY 3048 GCATTCGTCTCTGAGCGGACCATCAAGAGACTACAGGGAATATTGCTTGTGAAGACTGC 3107
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Db 373 GCATTCGTCTCTGAGCGGACCATCAAGAGACTACAGGGAATATTGCTTGTGAAGACTGC 432
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QY 3108 TCCAGTCTCTGATTCAGCAATATCCCAAGCAACCTGTTGATGTTGTTGAGC 3167
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Db 433 TCCAGTCTCTGATTCAGCAATATCCCAAGCAACCTGTTGATGTTGTTGAGC 492
|||||
QY 3168 AGCAGCTCTCTGATTCAGCAATATCCCAAGCAACCTGTTGATGTTGTTGAGC 3223
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Db 493 AGCAGCTCTCTGATTCAGCAATATCCCAAGCAACCTGTTGATGTTGTTGAGC 552
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QY 3224 -----GTATATGATTCCTTAAGT 3243
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Db 553 GAAAAAGCAATCCCTGGAACATGCTTAACTACAGTCAACATATGATTCCTTAAGT 612
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QY 3244 GTGAAGCTTAAGGCCCAAGATCAGAAAGGCCCAAGATCTTGTGATGCTTTCATC 3303
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Db 613 GTGAAGCTTAAGGCCCAAGATCAGAAAGGCCCAAGATCTTGTGATGCTTTCATC 672
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QY 3304 CTGAGGAATGCAAGGAGTGTGGGGTGGCGGAGTCTCCAGCCAGACAGTCTCC 3363
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Db 673 CTGAGGAATGCAAGGAGTGTGGGGTGGCGGAGTCTCCAGCCAGACAGTCTCC 730
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QY 3364 TTCTGCTCCTCTGCTTTTGTATGCTCTTCTCAAGTGAAGTGAAGTCTCTCTTA 3423
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Db 731 CTCTGCTCCTCTGCTTTTGTATGCTCTTCTC-AGGGGAGACTGAGTGAAGTCTCTTTA 789
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QY 3424 CTGACTGAGATG 3435
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Db 790 CTGACTGAGATG 801
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RESULT 7
AV722352 608 bp mRNA linear EST 16-OCT-2000
LOCUS AV722352 HTB Homo sapiens cDNA clone HTBAVB10 5', mRNA sequence.
DEFINITION AV722352
VERSION AV722352.1 GI:10824752
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 608)
Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X.,
Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,
S., Gu,W., Tu,Y., Jia,D., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,
Chen,J., Chen,Z. and Han,Z.
Homo sapiens cDNA HTB clones
Unpublished (2000)
CONTACT: Zenguan Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@hgsc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source location/Qualifiers
1..608
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HTBAVB10"
/clone_lib="HTB"
/tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 159 a 150 c 141 g 157 t 1 others
ORIGIN

Query Match 15.5% Score 583.8; DB 10; Length 608;
Best Local Similarity 98.8%; Pred. No. 7,5e-91;
Matches 599; Conservative 0; Mismatches 3; Indels 4; Gaps 1;
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Db 1 GTGGAATTTAACTCTGAGTTGGGACATCCGATATGACAGTAAAGCCAGAAATTTG 60
|||||
QY 3012 AAACAGACCTTGAGACCTTTGATAGTAAATATCCAGATTCGTTCTGAGCGACATC 3071
|||||
Db 61 AAACAGACCTTGAGACCTTTGATAGTAAATATCCAGATTCGTTCTGAGCGACATC 120
|||||
QY 3072 AAGGACTACAGGGAATATGCTTGTGAAGAGCTCCAGAGTCTTTGTATGACAGAA 3131
|||||
Db 121 AAGGACTACAGGGAATATGCTTGTGAAGAGCTCCAGAGTCTTTGTATGACAGAA 180
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QY 3132 ATCCCAAGCAGCAACCTTTGATGTTGGTGTGAGACAGACCTGCTTGTGAATCTGTG 3191
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Db 181 ATCCCAAGCAGCAACCTTTGATGTTGGTGTGAGACAGACCTGCTTGTGAATCTGTG 240
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QY 3192 GCCCCATCACCATGCGACCCATTGAATAGATTAATGATCCCTTAAGTGAACGT 3251
|||||
Db 241 GCCCCATCACCATGCGACCCATTGAATAGATTAATGATCCCTTAAGTGAACGT 300
|||||
QY 3252 CTAAAGGCCCAAGATCAGAAAGGCCCGCAATCTTGTATGCTTGTGATCTGAGAG 3311
|||||
Db 301 CTAAAGGCCCAAGATCAGAAAGGCCCGCAATCTTGTATGCTTGTGATCTGAGAG 360
|||||
QY 3312 AATGCAAGGAGTGTGGGGTGGCGGAGTCTCCAGCCAGACAGTCTCTGCTC 3371
|||||
Db 361 AATGCAAGGAGTGTGGGGTGGCGGAGTCTCCAGCCAGACAGTCTCTGCTC 420
|||||
QY 3372 CCTCTGCTTTGATGCTCTTCTCAAGTGAAGTGAAGTCTTCTTACTGACTGA 3431
|||||
Db 421 CCTCTGCTTTGATGCTCTTCTCAAGTGAAGTGAAGTCTTCTTACTGACTGA 480
|||||
QY 3432 GATGTTCTCTTGTGATCTTAAATCATGATTAAGTGAACCAAAATATGTTGACATGA 3491
|||||
Db 481 GATGTTCTCTTGTGATCTTAAATCATGATTAAGTGAACCAAAATATGTTGACATGA 536
|||||
QY 3492 CGAGACATGATATAGTCAACCATCAGATCATCATGATTTTAAAGTGGCGATGA 3551
|||||
Db 537 CGAGACATGATATAGTCAACCATCAGATCATCATGATTTTAAAGTGGCGATGA 596
|||||
QY 3552 TAAACT 3557
|||||
Db 597 TAACT 602
|||||

RESULT 8
BG218214 762 bp mRNA linear EST 21-APR-2001
LOCUS BG218214
DEFINITION RST37941 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG218214
VERSION BG218214.1 GI:13744235
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 762)
Harrington,J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,
J., Veloso,N., Kika,A., Hess,J., Cohen,K., Lo,K., Offenbacher,
J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
CONTACT: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900
Fax: 216 361 9596

Email: scain@atherys.com
High quality sequence stop: 379.

FEATURES

Source

Location/Qualifiers

1. .762
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"

/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
expressed in HT1080 under normal circumstances."

BASE COUNT 205 a 165 c 186 g 205 t 1 others
ORIGIN

Query Match 14.9% Score 561.2; DB 12; Length 762;
Best Local Similarity 89.6% Pred. No. 5.5e-87;
Matches 682; Conservative 0; Mismatches 69; Indels 10; Gaps 7;

2635 AGGTGCTTCCCTGGATGCGCAATGCTTCATCAGCTGTGATGAGATCTGTGATTTGTT
|||||
2 AGTGTGTTCCCTGGATGCGCAATGCTTCATCAGCTGTGATGAGATCTGTGATTTGTT
|||||
2695 ACCTGATAGCAATTAATGATTTATTTGCTGTGAGACTACACAGACTGGAGACT 2754
|||||
62 ACCTGATAGCAATTAATGATTTATTTGCTGTGAGACTACACAGACTGGAGACT 121
|||||
2755 TTTTGGTGAGATCGAGGAGCTGTGATGAACAATGCTAACATGAGCTCTTAAAA 2814
|||||
122 TTTTGGTGAGATCGAGGAGCTGTGATGAACAATGCTAACATGAGCTCTTAAAA 181
|||||
2815 GAATTAACCTTTATGACTACCAAGCATGTGTAGAGCCAAACAGAAACAGCGATGGC 2874
|||||
182 GAATTAACCTTTATGACTACCAAGCATGTGTAGAGCCAAACAGAAACAGCGATGGC 241
|||||
2875 CCATGAGCTCTGTGATGCTTATATGCTCTGCTGTGAGTAATTAATGATGACAG 2934
|||||
242 CCATGAGCTCTGTGATGCTTATATGCTCTGCTGTGAGTAATTAATGATGACAG 301
|||||
2935 AACTTGTCTTGTCTGTGAGTAATTAATGCTCTGCTGTGAGTAATTAATGATGACAG 2994
|||||
302 AACTTGTCTTGTCTGTGAGTAATTAATGCTCTGCTGTGAGTAATTAATGATGACAG 361
|||||
2995 CTAAACCCAGAAATGAAACAGACCCCTGTGTGATGATGATGATGATGATGATG 3054
|||||
362 CTAAACCCAGAAATGAAACAGACCCCTGTGTGATGATGATGATGATGATGATG 421
|||||
3055 TCTGTAGGCGACATCAAGGAGACTACAGGGAATTAATGCTCTGCTGTGAGTAAT 3114
|||||
422 TTTCTAGGCGACATCAAGGAGACTACAGGGAATTAATGCTCTGCTGTGAGTAAT 481
|||||
3115 CTTTGTGATCGAACAATCCCAAGCAGCACTGTCA-TGGTGTGAGTGTGACAGCAGC 3173
|||||
482 CTTTGTGATCGAACAATCCCAAGCAGCACTGTCA-TGGTGTGAGTGTGACAGCAGC 541
|||||
3174 -TGGCTGTGATCTGTGAGCCCAT---CACCATGCAACCATTTGATGATGATGAT 3229
|||||
542 TTTGCTGTGAGTGTGAGCCCATTTGATGATGATGATGATGATGATGATGATGAT 601
|||||
3230 TGAATCCCTTAAGT--GTGACGCTTAAGGCCAGAGATCGAGAGGCGCC-AGAAATC 3286
|||||
602 TGAATCCCTTAAGTGGGAAAGCGCCAAAGGCCAAAGAGAGAGAGAGAGAGAGAG 661
|||||
3287 TTGTCAAT-GGCTTCATCTGTGAGAGAGATGCAAGGAGTGTGGGGGTGAGCCAGATCTCC 3345
|||||
662 TTGTCTTTGGGCTTCACTTCTGTGAGAGAAATGCAAGAGATGTGTGATGATGATGAT 721
|||||
3346 A-AGCCCAACAGTCTCTCTTGTGCTCTCTGCTTTTAA 3385
|||||

Db 722 AGAGCCAAAAGGCTACTTCTGCTCTCTGCTGTTTGAAT 762

RESULT 9

BM992229/c

LOCUS

644 bp mRNA linear EST 17-JUN-2002

DEFINITION UI-H-DPI-aub-h-16-0-UI-s2 NCI-CGAP-DPI Homo sapiens CDNA clone

IMAGE:5869503 3', mRNA sequence.

ACCESSION BM992229

VERSION BM992229.1 GI:19711618

KEYWORDS

EST.

SOURCE

ORGANISM

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/BLN at: http://image.llnl.gov

The following repetitive elements were found in this CDNA

sequence: 1-45, >AT-rich#low_complexity (matched complement)

Seq primer: M13 FORWARD

POLYA=yes.

FEATURES

Source

Location/Qualifiers

1. .644

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="IMAGE:5869503"

/clone_lib="NCI-CGAP-DPI"

/dev_stage="Adult"

/tissue_type="Subchondral Bone"

/lab_host="DH10B (Life Technologies)"

/note="Organ: Bone; Vector: pT73-Pac (Pharmacia) with a

modified polylinker. Site-1: EcoR I. Site-2: Not I;

NCI-CGAP-DPI is a normalized CDNA library containing the

following tissue(s): Subchondral Bone. The library was

constructed according to Bonaldo, Lennon and Soares,

Genome Research, 6:791-806, 1996. First strand CDNA

synthesis was primed with an oligo-dT primer containing a

Not I site. Double stranded CDNA was ligated to an EcoR I

adaptor, digested with Not I, and cloned directionally

into pT73-Pac vector. The oligonucleotide used to prime

the synthesis of first-strand CDNA contains a library tag

sequence that is located between the Not I site and the

(dT)18 tail. The sequence tag for this library is

GTAAAGCGTC.

TAG_LIB-UI-H-DPI

TAG_TISSUE-subchondral bone

TAG_SEQ-GTTAAGCGTC"

BASE COUNT 174 a 128 c 129 g 213 t

ORIGIN

Query Match 14.4% Score 543; DB 14; Length 644;

Best Local Similarity 100.0% Pred. No. 7.9e-84;

Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3226 ATAATGATCCCTTAAGTGTGAACGCTTAAGGCCCGAGAGATCAGAGGCGCCAGAAAT 3285
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543 ATAATGATCCCTTAAGTGTGAACGCTTAAGGCCCGAGAGATCAGAGGCGCCAGAAAT 484
|||||
3286 CTTGTGATGCGCTTCCATCTGTGAGAGAAATGCAAGGAGTGTGGGGGTGCGCCAGATCTCC 3345
|||||
483 CTTGTGATGCGCTTCCATCTGTGAGAGAAATGCAAGGAGTGTGGGGGTGCGCCAGATCTCC 424
|||||

Qy	3346	AAGCCGAGACAGTCCTCCTCTGCTCCCTCTGCTTTTGATGCTCTTCTCAAGGTGACACT	3405
Db	423	AAGCCGAGACAGTCCTCCTCTGCTCCCTCTGCTTTTGATGCTCTTCTCAAGGTGACACT	364
Qy	3406	GACTGAGATGTTCTCTTACTGACTGAGATGTTCTCTTGGCATGCTAAATCATGATTAAC	3465
Db	363	GACTGAGATGTTCTCTTACTGAGATGAGATGTTCTCTTGGCATGCTAAATCATGATTAAC	304
Qy	3466	TGTGAACCAAAATATGTGTCAACATACGAGACATGAAATATAGTCCAAACCATCAAGCATCTC	3525
Db	303	TGTGAACCAAAATATGTGTCAACATACGAGACATGAAATATAGTCCAAACCATCAAGCATCTC	244
Qy	3526	ATCAGATTTTAAACGTGCGTGATATTAACCTTTAAAGATATGTTGACAAAAAAGTTATC	3585
Db	243	ATCAGATTTTAAACGTGCGTGATATTAACCTTTAAAGATATGTTGACAAAAAAGTTATC	184
Qy	3586	TATCATCTTTTACTTGTGCGCAGTCATGCAAAATGTGAGTTTGGCCACATGATTAATCACCCCTT	3645
Db	183	TATCATCTTTTACTTGTGCGCAGTCATGCAAAATGTGAGTTTGGCCACATGATTAATCACCCCTT	124
Qy	3646	CATCAGAAATGGAGCGCAAGTGTGAGAGTGTCCCTCTGCTTGAACCATTAAGCAAC	3705
Db	123	CATCAGAAATGGAGCGCAAGTGTGAGAGTGTCCCTCTGCTTGAACCATTAAGCAAC	64
Qy	3706	CAATTTAAACGTGTACTTTTAAATAAGATATATTAAATCATTAACAAAAA	3765
Db	63	CAATTTAAACGTGTACTTTTAAATAAGATATATTAAATCATTAACAAAAA	4
Qy	3766	AAA 3768	
Db	3	AAA 1	

RESULT	10
LOCUS	B0329542/c
DEFINITION	MRA-EN0075
ACCESSION	B0329542
VERSION	B0329542.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 658)
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Brlones,M.R., Nagal,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsumura,A., Bates,G.S., Simpson,D.H., Grimstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare M,J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL MEDLINE COMMENT	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) Contact: Simpson A.J.G.

FEATURES
 source
 1. 658
 location/Qualifiers
 High quality sequence start: 117
 High quality sequence stop: 138.
 Seq primer: puc 18 forward.
 220101-006-104ct3+2001-01-22ct4-1)
 http://www.ludwig.org.br/scripts/gethtml2.pl?l1=MR&l2=MR4-EN0075-
 project. This entry can be seen in the following url
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Email: asimpson@ludwig.org.br
 Fax: +55-11-2707001
 Tel: +55-11-2704922
 Brazil
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Ludwig Institute for Cancer Research

```

/db_xref="taxon:9606"
/clone_lib="EN0075"
/dev_stage="Adult"
/note="Origin: lung-normal; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT      161 a      150 c      156 g      150 t      1 others
ORIGIN

```

Query Match	13.9%	Score 523.47	DB 14	Length 658
Best Local Similarity	89.4%	Pred. No. 1.9e-80		
Matches 585	Conservative	0	Mismatches 67	Indels 2
Qy	303	AAATCCATTGCTGCTAAGTACTCCGGTTCCAGCTTTCGCAAAAGAAATACAAAGAGTAT	362	
Db	654	AAATCCATGCTGCTAAGTACTCCGGTTCCAGCTTTCGCAAAAGAAATACCAAGATAT	595	
Qy	363	GAGAAAGACGTTGCCATTAAGAANAATGATGGCCCTCCAACTGCTAAAGAGCTGGCAAG	422	
Db	594	GAGAAAGACGTTGCCATTAAGAANAATGATGGCCCTCCAACTGCTAAAGAGCTGGCCAA	535	
Qy	423	AACATGGAAGAGATGTTTTCACAAGAAGTGTGAGGCCGTGACAGCGTCTGCTGGAGGCTCA	482	
Db	534	AACATGGAAGAGATGTTTTCACAAGAAGTGTGAGGCCGTGACAGCGTCTGCTGGAGGCTCA	475	
Qy	483	GAAAGAGCACACCTGAAACATGATTTGATGACAGCTTACAGTATGAATACTTCANTCT	542	
Db	474	GAAAGAGCACACCTGAAACATGATTTGATGACAGCTTACAGTATGAATACTTCANTCT	415	
Qy	543	GTGCTGATTAATGAAAGAGACCAAGACGGAGATTTTTGGAGCTGGGAAGAATTCATC	602	
Db	414	GTGCTGATTAATGAAAGAGACCAAGACGGAGATTTTTGGAGCTGGGAAGAATTCATC	355	
Qy	603	TTAGCCCCAATGACCATTATTAATATTTGCTGTGAACATCAGTCTAAGTACGCTCCAA	662	
Db	354	TTAGCCCCAATGACCATTATTAATATTTGCTGTGAACATCAGTCTAAGTACGCTCCAA	295	
Qy	663	GTACCAAGCAATGTACAAACAAGACCCCTGCAATTTGCATGGGGTTATTGGTCTGAA	722	
Db	294	GTACCAAGCAATGTACAAACAAGACCCCTGCAATTTGCATGGGGTTATTGGTCTGAA	235	
Qy	723	TCTCTAAACAAAGTTTTGTAGATTAACCTTGAACCGTGAACCCATCTCTCATATGCGAGTAC	782	
Db	234	TCTCTAAACAAAGTTTTGTAGATTAACCTTGAACCGTGAACCCATCTCTCATATGCGAGTAC	175	
Qy	783	TTTGAAGTGCAGAAAGGCTTTTATAGCAGATATCCGGGATTAATATGGAACCAAGATGAG	842	
Db	174	TTTGAAGTGCAGAAAGGCTTTTATAGCAGATATCCGGGATTAATATGGAACCAAGATGAG	115	
Qy	843	AATGAGTCAATTTGCCCTTGACCTGACAG-GAACCGAAATATGTATCCAGCAGCAGC-NACTT	900	
Db	114	AATGAGTCAATTTGCCCTTGACCTGACAG-GAACCGAAATATGTATCCAGCAGCAGC-NACTT	55	
Qy	901	CTCCGAAGAGAGCTGCTATTTAGTTGACGTGACGTGGCAGCAGTAAGAAGACTCC	954	
Db	54	TTCCGGTAAACTGCTGCTATTTAGTTGACGTGACGTGGCAGCAGTGAACGAGACTCC	1	

RESULT 11

LOCUS B1736456

DEFINITION 799 bp mRNA linear EST 20-SEP-2001

ACCESSION B1736456

VERSION B1736456.1 GI:15713469

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 799)	Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; Mus			
NIH-MGC http://mgc.ncbi.nlm.nih.gov/ .				
National Institutes of Health, Mammalian Gene Collection (MGC)				
Unpublished (1999)				
Contact: Robert Strausberg, Ph.D.				

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FEATURES
Source
Location/Qualifiers
1. 799
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:5366518"
/clone_1lb="NIH_MGC_94"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCNAW-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dt primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies Note: this is a NIH_MGC Library."
BASE COUNT
191 a 211 c 187 g 210 t
ORIGIN

```

Db	656	CGTCCAGANCTCTGCCACGG - TTCCATCTGTGAGGAGAAATGCAAGAGAGTGTGGGGTGTGA	714
Qy	3336	CCGAGTCTCCAGAGCCCAAGACAGCTCCCTCTTGCTGCTCCCTCTCTTTGATGCTCTTCTCA	3395
Db	715	TCGAGTCTTCACAGGCCCAAGCGGGCTTGCTGCTGCTGCCCTGGTTTCGATCTCTTTCTCA	774
Qy	3396	AGGTGACACTGACTGA	3411
Db	775	AGGTGACACTAATAA	790

Matches 599: Conservative 0; Mismatches 71; Indels 12; Gaps 3;

```

QY 96 CGGCGGCTCTGTCGCGCCGCGAGGCGGCTGCGAGGAGACCCAGCATGCGCGCGG 155
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 CGGCGGCTCTGTCGCGCCGCGAGGCGGCTGCGAGGAGACCCAGCATGCGCGCGG 50
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 156 GGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 215
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 51 GGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 110
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 216 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 275
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 111 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 170
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 276 TGGCGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 335
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 171 TGGCGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 230
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 336 CTCTGCGAAAGAAATACAAAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAG 395
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 231 CTCTGCGAAAGAAATACAAAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAG 290
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 396 CTCTGCGAAAGAAATACAAAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAG 455
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 291 CTCTGCGAAAGAAATACAAAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAG 350
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 456 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 515
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 351 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 410
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 516 GACTTACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 575
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 411 GACTTACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 470
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 576 TTTTGGAGCTGGGAAAGAAATATCATCTTATGAGGCGGCGGCGGCGGCGG 635
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 471 TTTTGGAGCTGGGAAAGAAATATCATCTTATGAGGCGGCGGCGGCGGCGG 529
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 636 GTGACATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 695
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 530 GTGACATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 589
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 696 ATTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 754
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 590 ATTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 649
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 755 CCGTGACCATCTCTCATATGAG 776
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 650 CCGTGACCATCTCTCATATGAG 671
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 13
BM949850 618 bp mRNA linear EST 14-MAR-2002
LOCUS UT-M-EGOP-buv-18-0-UT.r1 NIH_BMAP_EGop Mus musculus cDNA clone
DEFINITION IMAGE:5687873 5', mRNA sequence.
ACCESSION BM949850
VERSION BM949850.1 GI:19433440
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 618)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: PYX-5.

FEATURES

source Location/Qualifiers
1. 618
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:5687873"
/clone_id="NIH_BMAP_EGop"
/tissue_type="whole brain"
/dev_stage="embryo 18.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/note="Organ: brain; Vector: PYX-Asc; Site:1: EcoR I; Site:2: Not I; The library was constructed according to Bonaldi, Lennon and Soares, genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then sequenced directionally into PYX-Asc vector. The library tag is CAGCCAGCAGC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemlin Chlin, Ph.D., Program coordinator."

BASE COUNT 182 a 140 c 153 g 141 t 2 others
ORIGIN

Query Match 13.3%; Score 500.6; DB 14; Length 618;
Best local Similarity 88.9%; Pred. No. 1.6e-76;

Matches 550; Conservative 1; Mismatches 67; Indels 1; Gaps 1;

```

QY 1640 AGTGAAGAAGCTTCTGAGACATCCCAATACAGTTAGGATTCACGGTTATGCTT 1699
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 AGTTAAGAGCTTCTGAGACATCCCAATACAGTTAGGATTCACGGTTATGCTT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1700 TCGAATCACAAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1759
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 CGCATCAGCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1760 AGGAAAAAGCGAAGAACTAATGATGATGATGATGATGATGATGATGATGATGAT 1819
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 A-AAAAAAGCGAAGAACTAATGATGATGATGATGATGATGATGATGATGATGAT 179
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1820 AGACGAGATGACGTTGAGAAATGCTATGATGATGATGATGATGATGATGATGAT 1879
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 180 AGACGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 239
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1880 GGAGGTGAAGAGACAGTGCACAAAGGAAACGGCTTTGGTGTGATGACAAATGACTACTA 1939
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 240 GGAATGGAAGAGACAGTGCACAAAGGAAACGGCTTTGGTGTGATGACAAATGACTACTA 299
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1940 TTATACAGACATCAAGGGTACTCTTTAGTTAGTGGCGCTTCCACAGTCAATG 1999
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 300 CTATACAGACATCAAGGGTACTCTTTAGTTAGTGGCGCTTCCACAGTCAATG 359
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2000 GAAATATTTCTTCCGAGGAAATGTAACCATGGAAGAGCGCTGCATGACTAGAACATCC 2059
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 360 GAAATATTTCTTCCGAGGAAATGTAACCATGGAAGAGCGCTGCATGACTAGAACATCC 419
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2060 CGATGTCCTCTTGGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2119
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 420 TGAGCTGCTCTTGGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 479
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2120 CCATCTGCTCAGTTAGAGGATTAAGCTTAAAGCGAAAGAACCTGCTGCTCA 2179
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 480 CCATCTATCTCACTGGAAGCGATTAAGCTTAAAGCGAAAGAACCTGCTGCTCA 539
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

Oy	2180	GGTGTTAAAGATTCATCCAGCAACTCCTTTTGGACGGGGTGCGTAG;GCCCCATTGA	2239
Dd	540	ATGTGCACAAGAATTATTCACAGACGCTCTTTTGATGCTGTGGTAG;GCCCCATTGA	599
Oy	2240	AGCGTAATTGAGCACCGCTG	2258
Dd	600	AGCCTATTGGACGAGCCTG	618
RESULT 14			
B1736450			
LOCUS			
DEFINITION	B1736450	711 bp	mRNA
	603359485F1 NIH_MGC_94	Mus musculus	CDNA clone IMAGE:5366516 5'
			mRNA sequence.
ACCESSION	B1736450		
VERSION	B1736450.1	GI:15713463	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 711)		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strusberg, Ph.D. Email: rgsrbs@mail.nih.gov Tissue Procurement: The Cepko Laboratory CDNA Library Preparation: Life Technologies, Inc. CDNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnln.gov Plate: LLM11932 row: j column: 21 High quality sequence stop: 709. Location/Qualifiers 1..711		
FEATURES			
source			

QY	2976	TGGCACTCCGAATATACAGACTAAAGCCCGAATAATGAAACACACCTGTGAGCTTGTGAT	3035
Db	354	TGGCACTCCGAATATACAGACTAAAGCCCGAATAATGAAACACACCTGTGAGCTTGTGAT	413
QY	3036	ACTGAATATCCAGATTCGTCTCTGTAGGCGACCATCAAGGAGACTACAGGAATATTGCT	3095
Db	414	ACTGAATATCCAGATTCGTCTCTGTAGGCGACCATCAAGGAGACTACAGGAATATTGCT	473
QY	3096	TGTGAAGACTGTCCAAAGTCCTTTGTTCATCCAGCAAAATCCAGCAGCAACCTGTTTCATG	3155
Db	474	TGTGAAGACTGTCCAAAGTCCTTTGTTCATCCAGCAAAATCCAGCAGCAACCTGTTTCATG	533
QY	3156	GTGGAGGAGGAGCAGCAGGTCGCTCTGTGAATCTGTGGCCCCCATATACCATGTGCACCCATT	3215
Db	534	GTGGAGGAGGAGCAGCAGGTCGCTCTGTGAATCTGTGGCCCCCATATACCATGTGCACCCATT	593
QY	3216	GAATACAGATTAATGAATCCCTTAAGTGTGAAGCTTAAGAGGCCACAGAAGTCGGAAGG	3275
Db	594	GAATACAGATTAATGAATCCCTTAAGTGTGAAGCTTAAGAGGCCACAGAAGTCGGAAGG	653
QY	3276	CGCCCAAGATCTTGTTCATCAGGCTTCCATCCTAGAGAGAAATGCAAGGAGATGTGGGGGTG	3333
Db	654	CGTCAGAAATCTCGCCACAGGTTTCCATCTCAGAGGAATGCAAGGAGATGTGGGGGTG	711

RESULT	15
BFA65072	
LOCUS	BFA65072 589 bp mRNA linear EST 04-DEC-2000
DEFINITION	UI-M-CGDb-bqg-d-09-0-UI.s1 NIH_BMAP_Ref4_s3 Mus musculus cDNA clone
ACCESSION	UI-M-CGDb-bqg-d-09-0-UI 3', mRNA sequence.
VERSION	BFA65072
KEYWORDS	BFA65072.1 GI:11534255
SOURCE	EST.
ORGANISM	house mouse,
	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathl; Muridae; Murinae; Mus. 1 (bases 1 to 589)
ATTACHED	

FEATURES
source

Query Match	Best Local Similarity	Matches 53%;	Conservative	Score 13.18;	DB 13;	Length 711;
				Pred. No. 49-75;	Mismatches 66;	Indels 0;
						Gaps 0;
Y 2736	TACACACAGACTGCAGACTTTTTTTGGTGAATCGAGGAGCTGTGATGAACAAATTGCTA	178 a	185 c	162 g	186 t	
Db 114	TCCCTACAGACTGCAGATTTTGTGGAGGTGGAGGAGCTGTGATGAACAACTGTTA					
Y 2796	ACATGGCGCTCTTTAAAGAAATTTACCTTTATGACTACCAAGCCATGTGTAGAGCCAAC					
Db 174	ACATGGCGCTCTTTAAAGAAATTTACCTTTATGACTACCAAGCCATGTGTAGAGCCAAC					
Y 2856	AAGGAAGCAGCAGTGGCGGCCCAATGGCGCTCCGTGATCTTAAATGTCCTTCTCTGCA					
Db 234	AAGGAGAGCAGTGCACATGCGCCATGGACTCTGTGAGCCCATTAAGGCGCTTCTCTGCA					
Y 2916	GTAATATGATCATTCAGACAGAACTGTCTTCTGCTGGTGAATTTAAACCTCTGCAGTTGG					
Db 294	GCCAGTGGATATATGACAGGAACCTTGTCTTCTGTGGTGAATTTAAACCTCTGCAGTTGG					

FEATURES
 SOURCE
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7150, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mst@nml.nih.gov
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a Donalide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo-dT track served to identify it as a clone from the
 retina tissue cDNA Library Preparation: M.B. Soares Lab Clone
 GENETICS. It should be noted that Bento Soares from RESEARCH
 small number of additional specialized non-redundant arrays of BMAP
 cDNAs whose availability will be considered under appropriate and
 limited collaborative arrangements
 Seq primer: M13 Forward
 POLYA=Yes.
 Location/Qualifiers
 1. 589
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-CGP-bqg-d-09-0-UI"
 /clone_lib="NIH_BMAP_Ret4.S2"
 /lab_host="DH10b (Life Technologies)"
 /note="Vector: pT73D-pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; The

NIH-BMAP-Ret4_S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu. The tissue
for this library was contributed by Dr. Xin-Yuan Fu, Yale
University School of Medicine
TAG-LIB-NIH-BMAP-Ret4_S2
TAG-TISSUE-adult-retina
TAG-SEQ-GTCAGCGCGCAC"

BASE COUNT 156 a 134 c 147 g 152 t
ORIGIN

Query Match 12.7%: Score 479.4; DB 12: Length 589;
Best Local Similarity 89.4%: Pred. No. 7.4e-73;
Matches 516: Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 2754 TTTTGTGAGATCGAGGAGCTGTGATGAACAATGCTAACATGGCTCTTTAA 2813
DB 13 TTTTGTGAGGTCGAGAGAGCTGTGATGAACAATGCTAACATGGCTCTTTAA 72
QY 2814 AGAATTACCTTTATGACTACCAAGCCATGTGTAGAGCCCAAGAAAGCAGCATGCC 2873
DB 73 AGAATTACCTTTATGACTACCAAGCCATGTGTAGAGCCCAAGAAAGCAGCATGCC 132
QY 2874 GCCCATGGCTCTGTGATCTTATTAATGCTCTGTCAGTAAATGATCATGACA 2933
DB 133 GCCCATGGCTCTGTGATCTTATTAATGCTCTGTCAGTAAATGATCATGACA 192
QY 2934 GAATTTGCTTGTCTGTGTGGAATTTAATCTGTGACAGTGTGGCCTCCATATGACA 2993
DB 193 GAATTTGCTTGTCTGTGTGGAATTTAATCTGTGACAGTGTGGCCTCCATATGACA 252
QY 2994 GCTAAGCCCGAATTAAGAAACAGACCTGAGGCTGTGTACTGAATATCCAGCATTC 3053
DB 253 GCTAAGCCCGAATTAAGAAACAGACCTGAGGCTGTGTACTGAATATCCAGCATTC 312
QY 3054 GTCCTGAGGCGACCATCAAGAGACTACAGGAATATGCTGTGAAGACTGCTCCAG 3113
DB 313 GTCCTGAGGCGACCATCAAGAGACTACAGGAATATGCTGTGAAGACTGCTCCAG 372
QY 3114 TCCCTTGTCAATCCAGCAATCCAGCAGCAACCTGTTCAATGTGTGTGAGCAGCAGC 3173
DB 373 TCCCTTGTCAATCCAGCAATCCAGCAGCAACCTGTTCAATGTGTGTGAGCAGCAGC 432
QY 3174 TGCCTGTGAATCTGTGGCCCATCACCATGGCACCATTGAAATCAGTATATGAA 3233
DB 433 TGCCTGTGAATCTGTGGCCCATCACCATGGCACCATTGAAATCAGTATATGAA 492
QY 3234 TCCCTTAAGTGTGAGCTCTTAAGGCCAGAGATCAGAGGCCGCCAGAAATCTGTGCAT 3293
DB 493 TCCCTTAAGTGTGAGCTCTTAAGGCCAGAGATCAGAGGCCGCCAGAAATCTGTGCAT 552
QY 3294 GCGTTCATCTCTGAGAGAAATGCAAGGAGCTGTGGG 3330
DB 553 GCGTTCATCTCTGAGAGAAATGCAAGGAGCTGTGGG 589

Search completed: April 28, 2003, 01:17:00
Job time : 4644 secs

[illegible]

Db	1741	TCAGGTCGCTGTACGAAGAAAGAAAAAGCAAGGAACCTA	CTACTAGTACGCTTGACC	1800
Qy	1801	TCCTCTAGAGGTGGAGTGGGAAGACCGAGATGACGTGTTG	AAGATGCTATGGGTAAATGCAA	1860
Db	1801	TCCTCTAGAGGTGGAGTGGGAAGACCGAGATGACGTGTTG	AAGATGCTATGGGTAAATGCAA	1860
Qy	1861	AGACGGGGGAAGTCTTCCATGSGAGGTGAAGAAGACAGT	GGACCAAGGGAAACGGGTTTTGG	1920
Db	1861	AGACGGGGGAAGTCTTCCATGSGAGGTGAAGAAGACAGT	GGACCAAGGGAAACGGGTTTTGG	1920
Qy	1921	TCATGACAAATGACCTACTATTTATACAGACATCAAGGT	ACTCCCTTACAGTTAGTGTGG	1980
Db	1921	TCATGACAAATGACCTACTATTTATACAGACATCAAGGT	ACTCCCTTACAGTTAGTGTGG	1980
Qy	1981	CGCTTTCCAGAGGTTCATGGGAAATATTTCTCCGAGGGAA	TGTAAACCATGGAAGAGGCC	2040
Db	1981	CGCTTTCCAGAGGTTCATGGGAAATATTTCTCCGAGGGAA	TGTAAACCATGGAAGAGGCC	2040
Qy	2041	TGATGACTTGAACAATCCCGATGTGTCTTGGCAGATGA	TAATGTCTCTACTGCACACTG	2100
Db	2041	TGATGACTTGAACAATCCCGATGTGTCTTGGCAGATGA	TAATGTCTCTACTGCACACTG	2100
Qy	2101	ACCTACACCTTGAGCACCAGCTGTCTGATAGAGGATTA	AGCTCTACCTAAAG	2160
Db	2101	ACCTACACCTTGAGCACCAGCTGTCTGATAGAGGATTA	AGCTCTACCTAAAG	2160
Qy	2161	GCAGAAACCTCTGCTCCAGTGTGATTAAGAAATGATCCA	AAAGAGTCTCTTTTGGACGGG	2220
Db	2161	GCAGAAACCTCTGCTCCAGTGTGATTAAGAAATGATCCA	AAAGAGTCTCTTTTGGACGGG	2220
Qy	2221	TGCTGAGTGCCTCCCATTTGAAGCTATTTGGACACAGCT	GTGCGCTCAACAAATCTGAATTT	2280
Db	2221	TGCTGAGTGCCTCCCATTTGAAGCTATTTGGACACAGCT	GTGCGCTCAACAAATCTGAATTT	2280
Qy	2281	CTGACACAGGCGTGGAGGTGTGCTTCTCTGGCACTGSC	ACAGGGGCTCTCTCCAGATCAACC	2340
Db	2281	CTGACACAGGCGTGGAGGTGTGCTTCTCTGGCACTGSC	ACAGGGGCTCTCTCCAGATCAACC	2340
Qy	2341	TGTTTGTCTGGGGCTGAGCAGCTCACCAATCAGAGATCT	CTCGAAAGCTGGCGACAAAGAGA	2400
Db	2341	TGTTTGTCTGGGGCTGAGCAGCTCACCAATCAGAGATCT	CTCGAAAGCTGGCGACAAAGAGA	2400
Qy	2401	ACATTTTAAACGACACCATTTCCCTCTCTGTGATACCG	AAAGCGCGCTGAGCAGATTCACG	2460
Db	2401	ACATTTTAAACGACACCATTTCCCTCTCTGTGATACCG	AAAGCGCGCTGAGCAGATTCACG	2460
Qy	2461	GGAGCTCTGCTACCTGATGCCATTTCCATTTAGACACT	GTGGACATTAAGCAATGTGCTGA	2520
Db	2461	GGAGCTCTGCTACCTGATGCCATTTCCATTTAGACACT	GTGGACATTAAGCAATGTGCTGA	2520
Qy	2521	CAGCAAGTACATCCATCCAGCTCCCTGGATGAAGAGAA	ATTCCTCGTGGTGGCAGCTGTAG	2580
Db	2521	CAGCAAGTACATCCATCCAGCTCCCTGGATGAAGAGAA	ATTCCTCGTGGTGGCAGCTGTAG	2580
Qy	2581	GCATTCAGATGAACTTGAATTTTCCAAAGAAAGTTCT	GGACTGCGACAGACAGAGTGTG	2640
Db	2581	GCATTCAGATGAACTTGAATTTTCCAAAGAAAGTTCT	GGACTGCGACAGACAGAGTGTG	2640
Qy	2641	CTTCCCTGGATGGCAAAATGCTCCATCAGCTGTGATGA	TATAGACTGTGAATTTGTACTCTCA	2700
Db	2641	CTTCCCTGGATGGCAAAATGCTCCATCAGCTGTGATGA	TATAGACTGTGAATTTGTACTCTCA	2700
Qy	2701	TAGACAATTAATGATTTATTTTGGTGTGGAAGACTNCA	CACAGACAGACTGGAGACTTTTTTGG	2760
Db	2701	TAGACAATTAATGATTTATTTTGGTGTGGAAGACTNCA	CACAGACAGACTGGAGACTTTTTTGG	2760
Qy	2761	GTGAGATCGAGAGAGCTGTGATGAACAAATTTCTAACA	TATGGGCTCTTTAAAGAAATTA	2820
Db	2761	GTGAGATCGAGAGAGCTGTGATGAACAAATTTCTAACA	TATGGGCTCTTTAAAGAAATTA	2820
Qy	2821	CCCTTTATGACTTACCAAGCCATGTGTAGAGCCACAAG	AAAGAGCAGCGATGGCGCCCATG	2880
Db	2821	CCCTTTATGACTTACCAAGCCATGTGTAGAGCCACAAG	AAAGAGCAGCGATGGCGCCCATG	2880

D	b	2821	CCCTTTATGACTACCAAGCCATGTGTAGACCAACAAGAAACACGATGGCGCCANTG	2881
Q	y	2881	GCCTCTGGATCCTTATATATGCTTCCTCTCTGCTGACGTAAATAGATCATGACAGACTTG	2940
D	b	2881	GCCTCTGGATCCTTATATATGCTTCCTCTCTGCTGACGTAAATAGATCATGACAGACTTG	2940
Q	y	2941	TCTTTTCCCTGGTGGAAATTTAACTCTGACAGTTGGTGGCACTCCGATATGACAGCTAAAG	3000
D	b	2941	TCTTTTCCCTGGTGGAAATTTAACTCTGACAGTTGGTGGCACTCCGATATGACAGCTAAAG	3000
Q	y	3001	CCGAGAAATTAAGACAGACCCCTGGAGCCTTGATATCTGAAATATCCAGATTCGATCTCG	3060
D	b	3001	CCGAGAAATTAAGACAGACCCCTGGAGCCTTGATATCTGAAATATCCAGATTCGATCTCG	3060
Q	y	3061	AGCGCACCATCAAGSAGACTACAGGGAATATTTGCTTGTGAGACTGCTCCAAAGTCCCTTGG	3120
D	b	3061	AGCGCACCATCAAGSAGACTACAGGGAATATTTGCTTGTGAGACTGCTCCAAAGTCCCTTGG	3120
Q	y	3121	TCATTCACAGCAATCCCAAGCAGCACTGTTCAATGTTGGTGGTGGACAGCACTGCTCT	3180
D	b	3121	TCATTCACAGCAATCCCAAGCAGCACTGTTCAATGTTGGTGGTGGACAGCACTGCTCT	3180
Q	y	3181	GGGAATCTGTGGCCCCCATCAACAATGGCACCCATTAATAATACGTTATATGAATCCCTTA	3240
D	b	3181	GGGAATCTGTGGCCCCCATCAACAATGGCACCCATTAATAATACGTTATATGAATCCCTTA	3240
Q	y	3241	AGTGTGAACGTCTTAAAGGCCAGAGAATCAAGAGGGGCCAGAACTTGTATGCTCTCC	3300
D	b	3241	AGTGTGAACGTCTTAAAGGCCAGAGAATCAAGAGGGGCCAGAACTTGTATGCTCTCC	3300
Q	y	3301	ATTCGAGAGAGAAATGCAAGGAGTGTGGGGGTGGCGCGAGTCTCCAAAGCCAGACAGTCC	3360
D	b	3301	ATTCGAGAGAGAAATGCAAGGAGTGTGGGGGTGGCGCGAGTCTCCAAAGCCAGACAGTCC	3360
Q	y	3361	TCCTTCTGCTCCCTCTGCTCTTTGATGCTCTTTCACAAAGGTGACACTGACATGATTTCTC	3420
D	b	3361	TCCTTCTGCTCCCTCTGCTCTTTGATGCTCTTTCACAAAGGTGACACTGACATGATTTCTC	3420
Q	y	3421	TTACGACTGAGATGTTCTCTGTGCATGCTAAATCATGATGATTAACGTGAACCAAAATAT	3480
D	b	3421	TTACGACTGAGATGTTCTCTGTGCATGCTAAATCATGATGATTAACGTGAACCAAAATAT	3480
Q	y	3481	GGTGCACATACGAGACATGATATATGTCACACCATCAGCATCTCATGATTTTAAAC	3540
D	b	3481	GGTGCACATACGAGACATGATATATGTCACACCATCAGCATCTCATGATTTTAAAC	3540
Q	y	3541	TGTGCGGTGATATTAACCTCTTAAAGATATGTTGACAAAAGTTATCTATCATCTTTTACT	3600
D	b	3541	TGTGCGGTGATATTAACCTCTTAAAGATATGTTGACAAAAGTTATCTATCATCTTTTACT	3600
Q	y	3601	TTTGCGAGCATGCAAAATGATGATTTGGCACATGATTAATACCCCTTCATCAGAAATGGGAC	3660
D	b	3601	TTTGCGAGCATGCAAAATGATGATTTGGCACATGATTAATACCCCTTCATCAGAAATGGGAC	3660
Q	y	3661	CGCAAGTGTGAGCAGTGTCCCTTCTGCTTGAACCACTATTTGAACCAATTTAAACCTGTG	3720
D	b	3661	CGCAAGTGTGAGCAGTGTCCCTTCTGCTTGAACCACTATTTGAACCAATTTAAACCTGTG	3720
Q	y	3721	TACTTTTAAATTAAGATATTTAAATCATATAAAAAAAAAAAAAAAAAAAAAA 3770	
D	b	3721	TACTTTTAAATTAAGATATTTAAATCATATAAAAAAAAAAAAAAAAAAAAAA 3770	
RESULT 2				
AASeq1414				
ID AASeq1414 standard; cDNA: 3770 BP.				
XX AASeq1414:				
XX AC				
XX DT 04-JUL-2001 (first entry)				
XX Human secreted soluble alpha2delta calcium channel subunit #11 cDNA.				

KW	Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW	alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
KW	gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
KX	filter binding assay; wheat germ lectin flashplate assay; ss.
OS	Homo sapiens.
XX	
XX	Key
FH	Location/Qualifiers
FT	144..3401
CDS	/*tag= a
FT	/product= "Alpha2delta calcium channel subunit #1"
FT	
XX	
PN	WO200119870-A2.
XX	
PD	22-MAR-2001.
XX	
PF	18-SEP-2000; 2000WO-EP09137.
XX	
PR	16-SEP-1999; 99US-0397550.
XX	
PA	(WARN) WARNER LAMBERT CO.
XX	
PI	Brown JP, Bertelli F;
XX	
DR	WPI; 2001-235262/24.
XX	P-PSDB; AAU01024.
XX	
PT	Calcium channel alpha2delta subunits, useful in e.g. SPA assays;
PT	Flashplate assays, Nickel flashplate assays, Filter binding assays or
XX	Wheat Germ Lectin Flashplate assays -
PS	Claim 24; Page 93-94; 16pp; English.

The present sequence encodes for human secreted calcium channel α 1 subunit #1 which is soluble and retains the functional characteristics of the full length or wild type α 1 subunit (AAU01025). From which it is derived. The invention relates to truncated α 1 subunit-2, α 1 subunit-3 or α 1 subunit-4 subunit soluble proteins which retain their affinity for radioactively labelled glutathione. The α 1 subunit is 1 of the components of the heteromultimeric voltage-dependent calcium channel (VCC) complexes present in neuronal and non-neuronal tissues including heart and skeletal muscle. Numerous soluble forms of the human calcium channel α 1 subunits (AAU01014-AAU01024 and AAU01033-AAU01038) and 5 soluble forms of the porcine calcium channel α 1 subunits (AAU01027-AAU01031) are described. The secreted soluble α 1 subunit may be used in assays e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate, filter binding or wheat germ lectin flashplate assays to detect or measure the binding or interaction of a ligand (e.g. gabapentin, L-Norleucine, L-Vallo-isoleucine, L-methionine, L-leucine, L-isoleucine, L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel α 1 subunit.

Query Match	100.0%	Score 3769.6	DB 22	Length 3770
Best Local Similarly	100.0%	Pred. No. 0		
Matches 3770	0	Mismatches	0	Gaps 0

QY	1	TACTATAGGGCGGGCCGGCAATTCTGGCACAGAGCGCGCGGAGCGGACGAGCAGGACGCCCGC	60
Db	1	TACTATATAGGGCGGGCGGCAATTCTGGCACAGAGCGCGCGGAGCGGACGAGCAGGACGCCCGC	60
QY	61	GGCGTCCGCCACCGCCCGGCTCCGGGCAAGCTCCCGCGGGCGGCTCTGTCGCCCGCCGAGC	120
Db	61	GGCGTCCGCCACCGCCCGGCTCCGGGCAAGCTCCCGCGGGCGGCTCTGTCGCCCGCCGAGC	120
QY	121	GGGCGCGCTCGGAGGAGGCCACGACATGGCCCGGGCGCGGAGCTGCGCGCGCGCTCCCGGG	180
Db	121	GGGCGCGCTCGGAGGAGGCCACGACATGGCCCGGGCGCGGAGCTGCGCGCGCGCTCCCGGG	180
QY	181	GGGCGCTCGGCGCTTCGTGCTGGCGCGGCTTCTACGCGCGGCTGGGGGAACTGTGTCGCT	240
Db	181	GGGCGCTCGGCGCTTCGTGCTGGCGCGGCTTCTACGCGCGGCTGGGGGAACTGTGTCGCT	240

Db	181	GGGGCTGGGGCTTTCGCTGGCGGGCTTCTCTAGCGCGGCTGCGGGAGCTGTGCCT	240
Qy	241	CGGAGCAGCAGATACCGCTCTCCGTGGTGAAGCTCTGGGCGCTGGCTTTTGGTGGGAGA	300
Db	241	CGGAGCAGCAGATACCGCTCTCCGTGGTGAAGCTCTGGGCGCTGGCTTTTGGTGGGAGA	300
Qy	301	TAAATATCATTTGCTGTAGTACTCCGGTCCGAGCTTCTGGCAAAAGAAATACAAAGACT	360
Db	301	TAAATATCATTTGCTGTAGTACTCCGGTCCGAGCTTCTGGCAAAAGAAATACAAAGACT	360
Qy	361	ATGAGAAAGCGTTGGCAGTAGAAGAAATTGATGGCCTCCAACTGTAAAGAACTGGCAA	420
Db	361	ATGAGAAAGCGTTGGCAGTAGAAGAAATTGATGGCCTCCAACTGTAAAGAACTGGCAA	420
Qy	421	AGAACATGGAGAGATGTTTCCACAGAAGTGAAGCCGTCAGGCGCTGTGGAGGCTG	480
Db	421	AGAACATGGAGAGATGTTTCCACAGAAGTGAAGCCGTCAGGCGCTGTGGAGGCTG	480
Qy	481	CAGAAACACACCCCTGMAACATGGAATTTGATGCAAGACTTACAGTATGATACCTTAATG	540
Db	481	CAGAAACACACCCCTGMAACATGGAATTTGATGCAAGACTTACAGTATGATACCTTAATG	540
Qy	541	CTGTGCTGTAATTAATAAAGGACAAAGACCGGAATTTTGGAGCGTGGGAAAGAAATTA	600
Db	541	CTGTGCTGTAATTAATAAAGGACAAAGACCGGAATTTTGGAGCGTGGGAAAGAAATTA	600
Qy	601	TCTTAGCCCAAAATGACATTTTATTAATTAATTTGCCCTGGAACATCACTTAAGTAGCTCC	660
Db	601	TCTTAGCCCAAAATGACATTTTATTAATTAATTTGCCCTGGAACATCACTTAAGTAGCTCC	660
Qy	661	AAGTACCAACGAACATGTACACAACAAAGCCCTGCAATTTGTCAATGGGTTTATTGGTCTG	720
Db	661	AAGTACCAACGAACATGTACACAACAAAGCCCTGCAATTTGTCAATGGGTTTATTGGTCTG	720
Qy	721	AATCTTAACAACATTTTGTAGATTAACTTTGACGCTGACCCGATCTGCATATGGCAGT	780
Db	721	AATCTTAACAACATTTTGTAGATTAACTTTGACGCTGACCCGATCTGCATATGGCAGT	780
Qy	781	ACTTTGGAAGTGCAAAGGGCTTTTGTAGCGAGTATCCGGGGATTAATGGAGACAGATG	840
Db	781	ACTTTGGAAGTGCAAAGGGCTTTTGTAGCGAGTATCCGGGGATTAATGGAGACAGATG	840
Qy	841	AGAAATGGAGTCAATTCCTTCACATGCAAGAACCGAAATGATCATCGACGACCACTT	900
Db	841	AGAAATGGAGTCAATTCCTTCACATGCAAGAACCGAAATGATCATCGACGACCACTT	900
Qy	901	CTCCGAAAGAGTGGTCAATTTAGTACGTCAGTCAGTGGCAGANTGAAGAGACCTCGTCTGA	960
Db	901	CTCCGAAAGAGTGGTCAATTTAGTACGTCAGTCAGTGGCAGANTGAAGAGACCTCGTCTGA	960
Qy	961	CTATCGCAGACAAACAGTCTCATCACTTTTGGATACACTTGGGGATGATGACTCTTCA	1020
Db	961	CTATCGCAGACAAACAGTCTCATCACTTTTGGATACACTTGGGGATGATGACTCTTCA	1020
Qy	1021	ACATATTTGCTTAATATGAGAGCTTCACTATGTGAACCTTGCCGTAATGGAACCTTTGG	1080
Db	1021	ACATATTTGCTTAATATGAGAGCTTCACTATGTGAACCTTGCCGTAATGGAACCTTTGG	1080
Qy	1081	TGGCAGCCGACAGCAACAAGAGCACTTCAAGGAGCATCTGGACAAACTTTTCGCA	1140
Db	1081	TGGCAGCCGACAGCAACAAGAGCACTTCAAGGAGCATCTGGACAAACTTTTCGCA	1140
Qy	1141	AAGCAATTGGAAATTTGGATATAGCTGTGAATGAGCCCTCAACATCTGAGTATTTCA	1200
Db	1141	AAGCAATTGGAAATTTGGATATAGCTGTGAATGAGCCCTCAACATCTGAGTATTTCA	1200
Qy	1201	ACCAACAGGAGCAAGAAAGTATCTGCAAGTACAGCCATCACTGCTCAATCACTATGGGCGG	1260
Db	1201	ACCAACAGGAGCAAGAAAGTATCTGCAAGTACAGCCATCACTGCTCAATCACTATGGGCGG	1260
Qy	1261	TGGACACTATGATACATCTTTTGCAAAATACAAATTTGGCCAGATCGAAAGGTTGCATCT	1320
Db	1261	TGGACACTATGATACATCTTTTGCAAAATACAAATTTGGCCAGATCGAAAGGTTGCATCT	1320

QY	1141	AAGGAATTGGAAATGTTGGATATAGCTCTGAATGAGCCTTCAACATCTTGAGTGAATTCCA	12001
Db	1141	AAGGAATTGGAAATGTTGGATATAGCTCTGAATGAGCCTTCAACATCTTGAGTGAATTCCA	12001
QY	1201	ACCACACGGGCAACGAAGATATGCGACGTACGCCATCTCATCTAACTGATGGGGCGG	12601
Db	1201	ACCACACGGGCAACGAAGATATCTCGCAGTCAGGCCATCATCTCAATCTGATGGGGGGG	12601
QY	1261	TGGACACTATGATACATCTTTTGCAAAATACAAATTTGGCCAGATCGAAGGTTGGCATCT	13201
Db	1261	TGGACACTATGATACATCTTTTGCAAAATACAAATTTGGCCAGATCTGAAGGTTGGCATCT	13201

Qy	1321	TCACATACCTATTGGAGCAGAGCGCTGCCTTTGGAGACAACAACTAAAGTGAATGGCTGTG	1380
Db	1321	TCACATACCTATTGGAGCAGAGCGCTGCCTTTGGAGACAACAACTAAAGTGAATGGCTGTG	1380
Qy	1381	CCAAACAAAGGATTTTTTAACCCAGATCTCCACTTGGCTGATGTGCAGAGAGATGTCAATG	1440
Db	1381	CCAAACAAAGGATTTTTTAACCCAGATCTCCACTTGGCTGATGTGCAGAGAGATGTCAATG	1440
Qy	1441	AATACCTTCAAGCTGTAGCCGGGCCAAAGTCATCGACACGAGACATGATGTGGTGGA	1500
Db	1441	AATACCTTCAAGCTGTAGCCGGGCCAAAGTCATCGACACGAGACATGATGTGGTGGA	1500
Qy	1501	CCGAACTTACATTGACAGCACTCTGACTGATATCAAGGGCCCGCTCTGATGACCACTG	1560
Db	1501	CCGAACTTACATTGACAGCACTCTGACTGATATCAAGGGCCCGCTCTGATGACCACTG	1560
Qy	1561	TAGCATGCGCTGTGTTTAACTAAGCAGAACCAACAGATGAAAGGGCATCTCTGGGAG	1620
Db	1561	TAGCATGCGCTGTGTTTAACTAAGCAGAACCAACAGATGAAAGGGCATCTCTGGGAG	1620
Qy	1621	TGGTTGGCAGAGATGTCCAGTGAAGAAACTTTCGAAAGACATCCCAATATACAAGTTAG	1680
Db	1621	TGGTTGGCAGAGATGTCCAGTGAAGAAACTTTCGAAAGACATCCCAATATACAAGTTAG	1680
Qy	1681	GGATTACAGCTTATGCCCTTTGGCAATCACAAAATATGSRATATCTGACGATCCGGAAC	1740
Db	1681	GGATTACAGCTTATGCCCTTTGGCAATCACAAAATATGSRATATCTGACGATCCGGAAC	1740
Qy	1741	TCAGGGCGCTGTACGAAAGGAAAAAGGGAAGAACTTAATATAGCTAGCGTTGACC	1800
Db	1741	TCAGGGCGCTGTACGAAAGGAAAAAGGGAAGAACTTAATATAGCTAGCGTTGACC	1800
Qy	1801	TCTCTGAGGTGAGTGGGGAAGACCGAGATGACCTGTGGAATATGATATGGTGAATCGAA	1860
Db	1801	TCTCTGAGGTGAGTGGGGAAGACCGAGATGACCTGTGGAATATGATATGGTGAATCGAA	1860
Qy	1861	AGACGGGGGAATTTTCCATGAGAGTGAAGAAGACAGTGGACAAGGGAACGGGTTTGG	1920
Db	1861	AGACGGGGGAATTTTCCATGAGAGTGAAGAAGACAGTGGACAAGGGAACGGGTTTGG	1920
Qy	1921	TGATGCAATATACATCTATTATACGACATCAAGGATACTCTTTCAGTTAGGTGG	1980
Db	1921	TGATGCAATATACATCTATTATACGACATCAAGGATACTCTTTCAGTTAGGTGG	1980
Qy	1981	CGCTTTCAGAGAGTCATGGGAAATATTTCTCCGAGGGAAATGAACCATCGAAGAGGCC	2040
Db	1981	CGCTTTCAGAGAGTCATGGGAAATATTTCTCCGAGGGAAATGAACCATCGAAGAGGCC	2040
Qy	2041	TGCATGACTTAAACATCCCGATGTGTCTTGGCAGATGAATAGTCTTAATCTCAACATG	2100
Db	2041	TGCATGACTTAAACATCCCGATGTGTCTTGGCAGATGAATAGTCTTAATCTCAACATG	2100
Qy	2101	ACCTACACCTTAGAACACCGCCATCTGTCTCAATTGAAGCGATTAAAGCTTAACCTAAAG	2160
Db	2101	ACCTACACCTTAGAACACCGCCATCTGTCTCAATTGAAGCGATTAAAGCTTAACCTAAAG	2160
Qy	2161	GCAAGAACCTCTGCTCCAGTGTGATTAAGAATTGATCCAGAAGTCTCTTTGACGGGG	2220
Db	2161	GCAAGAACCTCTGCTCCAGTGTGATTAAGAATTGATCCAGAAGTCTCTTTGACGGGG	2220
Qy	2221	TGGTAGTGGCCCCATTGAACGTAATGGACAGCTGGCCCTCAACAAATCTGAAATTT	2280
Db	2221	TGGTAGTGGCCCCATTGAACGTAATGGACAGCTGGCCCTCAACAAATCTGAAATTT	2280
Qy	2281	CTGACAAAGGGGTGGAGGTGCGCTTCCCTGGCACTCGACGGGCTCTCCAGAAATCAACC	2340
Db	2281	CTGACAAAGGGGTGGAGGTGCGCTTCCCTGGCACTCGACGGGCTCTCCAGAAATCAACC	2340
Qy	2341	TGTTTGTGGGGCTGAGAGCTCAACATCAAGGACTTCTGAAGGTGGTGGACAAAGGAGA	2400
Db	2341	TGTTTGTGGGGCTGAGAGCTCAACATCAAGGACTTCTGAAGGTGGTGGACAAAGGAGA	2400

QY	2401	ACATTTTAAACGACAGACCATTTCCCTCTCTGTGTATCCGAAAGGCCGCTGACACAGATTCCAG	2460
Db	2401	ACATTTTAAACGACAGACCATTTCCCTCTCTGTGTATCCGAAAGGCCGCTGACACAGATTCCAG	2460
QY	2461	GGAGCTTCGTACTCGATGCCATGCCATTGACGACCTGGACAGCTCAATTAAGCAATGTGGTAA	2520
Db	2461	GGAGCTTCGTACTCGATGCCATGCCATTGACGACCTGGACAGCTCAATTAAGCAATGTGGTAA	2520
QY	2521	CAGCAAGTACATCCATCCAGTCCCTGGATATACGGAAATTCCTGTGGTGGCAGCTGTAG	2580
Db	2521	CAGCAAGTACATCCATCCAGTCCCTGGATATACGGAAATTCCTGTGGTGGCAGCTGTAG	2580
QY	2581	GCATTTCAGATGAACCTTGAAATTTTCCAAAGAAAGTTCTGAGCTGCCACAGACAGTGTG	2640
Db	2581	GCATTTCAGATGAACCTTGAAATTTTCCAAAGAAAGTTCTGAGCTGCCACAGACAGTGTG	2640
QY	2641	CTTCCCGAGATGGCAATGCTCCATACGCTGTATATGAGACTGTGAATGTACTTCA	2700
Db	2641	CTTCCCGAGATGGCAATGCTCCATACGCTGTATATGAGACTGTGAATGTACTTCA	2700
QY	2701	TAGACAAATATGATTTAATTTTGGTGTCAAGACATACACAGATCCGAGACTTTTTG	2760
Db	2701	TAGACAAATATGATTTAATTTTGGTGTCTGTAGACATACACAGATCCGAGACTTTTTG	2760
QY	2761	GTCGATGTCGAGGAGCTGTGTATGAACAAATTTGCTTAACAATGGGCTCTTTAAAGAAATTA	2820
Db	2761	GTCGATGTCGAGGAGCTGTGTATGAACAAATTTGCTTAACAATGGGCTCTTTAAAGAAATTA	2820
QY	2821	CCCTTTATGACTACCAAGCATGTGTAGAGCCAAACAGAAAGACAGATGGCGCCCATG	2880
Db	2821	CCCTTTATGACTACCAAGCATGTGTAGAGCCAAACAGAAAGACAGATGGCGCCCATG	2880
QY	2881	GCCTCTCGAATCCTTTAAATGGCTTCCTCTGTGCAAGTAAATGATTCATGACAGAACTTG	2940
Db	2881	GCCTCTCGAATCCTTTAAATGGCTTCCTCTGTGCAAGTAAATGATTCATGACAGAACTTG	2940
QY	2941	TCTTTGTCTGTGTGAATTTAAACCTCTGCAGTTGGTGGCAGCTCCGATATGACAGCTAAG	3000
Db	2941	TCTTTGTCTGTGTGAATTTAAACCTCTGCAGTTGGTGGCAGCTCCGATATGACAGCTAAG	3000
QY	3001	CCGAGAAATTTGAACACAGACCCCTGGAGCCTTGTGATCTGAATATTCACAGATTCGTCCTG	3060
Db	3001	CCGAGAAATTTGAACACAGACCCCTGGAGCCTTGTGATCTGAATATTCACAGATTCGTCCTG	3060
QY	3061	AGGCGACCATCAAGGAGACTACAGGAAATATGCTGTGGAGACTGCTCCAAAGTCTTTG	3120
Db	3061	AGGCGACCATCAAGGAGACTACAGGAAATATGCTGTGGAGACTGCTCCAAAGTCTTTG	3120
QY	3121	TCATCCAGCAAAATCCCAAGCAGCAACCTGTCATGAGTGTGTGGAGCAGCAGCTGCCCT	3180
Db	3121	TCATCCAGCAAAATCCCAAGCAGCAACCTGTCATGAGTGTGTGGAGCAGCAGCTGCCCT	3180
QY	3181	GTGAATCTGTGGCCCCCATCACCATGGCAGCCCATTTGAATCAGGTATATGAATCCCTTA	3240
Db	3181	GTGAATCTGTGGCCCCCATCACCATGGCAGCCCATTTGAATCAGGTATATGAATCCCTTA	3240
QY	3241	AGTGTGAACGCTTAAGGCCCGAAGAAATCAAAAGGCCCCAGAAATCTTGTGCATGGCTTC	3300
Db	3241	AGTGTGAACGCTTAAGGCCCGAAGAAATCAAAAGGCCCCAGAAATCTTGTGCATGGCTTC	3300
QY	3301	ATCTGTAGAGAGAAATGCAAGGAGTGTGGGGTGTGGCGGAGCTTCACAGCCCAACAGTCC	3360
Db	3301	ATCTGTAGAGAGAAATGCAAGGAGTGTGGGGTGTGGCGGAGCTTCACAGCCCAACAGTCC	3360
QY	3361	TCCTTCTCTCTCCCTCTGTCTTTTGATGCTCTTTCAGGTGACACTGACAGTGAATGTTCTC	3420
Db	3361	TCCTTCTCTCTCCCTCTGTCTTTTGATGCTCTTTCAGGTGACACTGACAGTGAATGTTCTC	3420
QY	3421	TTACGACTGTGATGTTCTCTGTGGCAATGCAATATCATGATTAACACTGTGAACCAAAATAT	3480
Db	3421	TTACGACTGTGATGTTCTCTGTGGCAATGCAATATCATGATTAACACTGTGAACCAAAATAT	3480
QY	3481	GGTGCACATACGAGACATGAATATATGCTCAACCATCAGATCTCATGATTTTAAAC	3540

Db 268 CATAGAAAGAAATTGATGGCTCCAACTGTTAAAGAGCTGGCAAGAAATATGGAAGAGAT 321
Qy 437 GTTTCACAAAGACTGTGAGGCCGTGCAGGCCGTGTGTGGAGCTGCAGAAAGACACCT 496
Db 322 GTTTCACAAAGACTGTGAGGCCGTGCAGGCCGTGTGTGGAGCTGCAGAAAGACACCT 381
Qy 497 GAAACATGAATTTGATGACAGACTTACAGTATGAAATCTTCAATGCTGTGATAAATGA 556
Db 382 GAAACATGAATTTGATGACAGACTTACAGTATGAAATCTTCAATGCTGTGATAAATGA 441
Qy 557 AAGGCAAAAGAGCGGGAATTTTGGAGCGGGAAGGAATTCATCTTACCCTCAATGA 616
Db 442 AAGGCAAAAGAGCGGGAATTTTGGAGCGGGAAGGAATTCATCTTACCCTCAATGA 501
Qy 617 CCATTTTAATTAATTTGCTGTGTGAACATCACTAAGTACGCTCAAGTACCAAGCAAT 676
Db 502 CCATTTTAATTAATTTGCTGTGTGAACATCACTAAGTACGCTCAAGTACCAAGCAAT 561
Qy 677 GTTCAACAAAGACCTTGCAATTTGTCAATGGGGTTTATGGTGTGAATCTTAAACAAAGT 736
Db 562 GTTCAACAAAGACCTTGCAATTTGTCAATGGGGTTTATGGTGTGAATCTTAAACAAAGT 621
Qy 737 TTTTGTAGTAACTTTGACCGGTGACCCATCTCATATGGCACTACTTTGGAAGTGCATA 796
Db 622 TTTTGTAGTAACTTTGACCGGTGACCCATCTCATATGGCACTACTTTGGAAGTGCATA 681
Qy 797 GGGCTTTTGTAGCACTATCCGGGGATTAATGGGAACCATGAGAAATGGAATCATTTGC 856
Db 682 GGGCTTTTGTAGCACTATCCGGGGATTAATGGGAACCATGAGAAATGGAATCATTTGC 741
Qy 857 CTTCGACTGAGAGACCGAAATGTGATCCAGGACGAATCTTCGAAAGACGTGT 916
Db 742 CTTCGACTGAGAGACCGAAATGTGATCCAGGACGAATCTTCGAAAGACGTGT 801
Qy 917 CATTTAGTGTGACGTGAGGAGGACATGAAAGACCTCCGTGACATATGCGGAAGCAAC 976
Db 802 CATTTAGTGTGACGTGAGGAGGACATGAAAGACCTCCGTGACATATGCGGAAGCAAC 861
Qy 977 AGTCTCATCTTTTGGATATGATACACTTGGGGATGATGACTTCTTCAACATATTTCTTATA 1036
Db 862 AGTCTCATCTTTTGGATATGATACACTTGGGGATGATGACTTCTTCAACATATTTCTTATA 921
Qy 1037 TTAGGAGCTTCTCATGTGTGAACCTTGGCTGAATGGAACCTTTGGTGAAGCCGACAGAG 1096
Db 922 TTAGGAGCTTCTCATGTGTGAACCTTGGCTGAATGGAACCTTTGGTGAAGCCGACAGAG 981
Qy 1097 AAACAAAGAGCACTTCAGGAGCATCTGACAAACTTTTCCGCCAAAGGAATTTGGAATTT 1156
Db 982 AAACAAAGAGCACTTCAGGAGCATCTGACAAACTTTTCCGCCAAAGGAATTTGGAATTT 1041
Qy 1157 GGATATAGCTGTGAATGAGGCGCTTCAACATTTGTAGTGTATTTCAACCAACAGGGAAGG 1216
Db 1042 GGATATAGCTGTGAATGAGGCGCTTCAACATTTGTAGTGTATTTCAACCAACAGGGAAGG 1101
Qy 1217 AAGTATTCGACGTCAAGCCATCATCTCATATACTGATGGGGGGGTGACACCTATGATAC 1276
Db 1102 AAGTATTCGACGTCAAGCCATCATCTCATATACTGATGGGGGGGTGACACCTATGATAC 1161
Qy 1277 AATCTTTGCAAAATATCAATTTGGCCAGATCGAAGAGTTGGCATCTTCACTATTTGG 1336
Db 1162 AATCTTTGCAAAATATCAATTTGGCCAGATCGAAGAGTTGGCATCTTCACTATTTGG 1221
Qy 1337 AAGAGAGGCTGCTTGTGAGACAAATCTAAAGTGTGATGGCTGTGCAACAAAGGATTTT 1396
Db 1222 AAGAGAGGCTGCTTGTGAGACAAATCTAAAGTGTGATGGCTGTGCAACAAAGGATTTT 1281
Qy 1397 TACCAAGATTCACACTTGGCTGATGTGCAGAGAGATGTCAATGAATACCTTCACGTGCT 1456
Db 1282 TACCAAGATTCACACTTGGCTGATGTGCAGAGAGATGTCAATGAATACCTTCACGTGCT 1341
Qy 1457 TAGCCGCGCCCAAGATCATCGACAGAGAGCATGATGTGTGTGAGCCGAA3CTTACATTGA 1516
Db 1342 TAGCCGCGCCCAAGATCATCGACAGAGAGCATGATGTGTGTGAGCCGAA3CTTACATTGA 1401

Qy 1517 CAGCACT-----CTGACTGATGATCAGGGCCGCTCCGTGATGACCAC 1558
Db 1402 CAGCACTCTCTCTCAGCACAAGAAAGCTGATGATGATCAGGGCCGCTCCGTGATGACCAC 1461
Qy 1559 TGTAGCCATGCTGTGTGTGTAGTAAAGCAGAAAGCAAGATCGAAGGCACTTCTTCTGGG 1618
Db 1462 TGTAGCCATGCTGTGTGTGTAGTAAAGCAGAAAGCAAGATCGAAGGCACTTCTTCTGGG 1521
Qy 1619 AGTGTGTGACAGATGTCCCAAGTGAAGAACTTGTGAAGACCATCCCAATATCAAGTT 1678
Db 1522 AGTGTGTGACAGATGTCCCAAGTGAAGAACTTGTGAAGACCATCCCAATATCAAGTT 1581
Qy 1679 AAGGATTCAGGCTTATGCTTGGCAATCAAAATTAAGGATATATCTGACGATCCGGA 1738
Db 1582 AAGGATTCAGGCTTATGCTTGGCAATCAAAATTAAGGATATATCTGACGATCCGGA 1641
Qy 1739 ACTCAGGCTCTGTAGCAGAAAGGAAAGAAAGCAAGAACTTAATATATGATGACCTTGA 1798
Db 1642 ACTCAGGCTCTGTAGCAGAAAGGAAAGAAAGCAAGAACTTAATATATGATGACCTTGA 1701
Qy 1799 CTTCTCTGAGGTGAGTGGGAGACGAGATGACGTTGTGAAGAAATGCTATGATGATCG 1858
Db 1702 CTTCTCTGAGGTGAGTGGGAGACGAGATGACGTTGTGAAGAAATGCTATGATGATCG 1761
Qy 1859 AAGAGCGGGGAATTTTCCATGAGGTGAAGAAAGACAGTGAACAAAGGCAACGGTTTT 1918
Db 1762 AAGAGCGGGGAATTTTCCATGAGGTGAAGAAAGACAGTGAACAAAGGCAACGGTTTT 1821
Qy 1919 GGTGATGACAAATGACTATATATACAGATCAAGGGGATCTCTTCAAGTTAGGTGT 1978
Db 1822 GGTGATGACAAATGACTATATATACAGATCAAGGGGATCTCTTCAAGTTAGGTGT 1881
Qy 1979 GGGCTTTTCCAGAGGTGATGGAATATTTCTTCCAGGGGAATGTAACCATGCAAGAG 2038
Db 1882 GGGCTTTTCCAGAGGTGATGGAATATTTCTTCCAGGGGAATGTAACCATGCAAGAG 1941
Qy 2039 CTTGCAATGACTTGAACATCTCCGATGTGCTTGTGAGAGATGAATGCTTCTACTGCAAC 2098
Db 1942 CTTGCAATGACTTGAACATCTCCGATGTGCTTGTGAGAGATGAATGCTTCTACTGCAAC 2001
Qy 2099 TGACTACACCCCTGAGACACCGCATCTGTCTGCTAGTAAAGGATTAATGCTTACTATAA 2158
Db 2002 TGACTACACCCCTGAGACACCGCATCTGTCTGCTAGTAAAGGATTAATGCTTACTATAA 2061
Qy 2159 AAGCAAAAGAACTTGTGCTCAGTGTGATAAAGAAATGATCAAGAAAGTCTTTTGGACG 2218
Db 2062 AAGCAAAAGAACTTGTGCTCAGTGTGATAAAGAAATGATCAAGAAAGTCTTTTGGACG 2121
Qy 2219 GGTGTGAGTGGCCCATTTGAAGCGTATTTGAACAGCCTGSCCTTCAACAAATCTGAAGA 2278
Db 2122 GGTGTGAGTGGCCCATTTGAAGCGTATTTGAAGCGCCTGSCCTTCAACAAATCTGAAGA 2181
Qy 2279 TTCTGACAAAGGCGTGTGAGAGTGTGCTTCTGTGGCACTGTGCAAGGGGCTCTCCAGAAATCAA 2338
Db 2182 TTCTGACAAAGGCGTGTGAGAGTGTGCTTCTGTGGCACTGTGCAAGGGGCTCTCCAGAAATCAA 2241
Qy 2339 CCTGTTTGTGCGGGGCTGAGACAGCTCACCAGTCAAGGACTTCTGAAAGCTGGGGAAGA 2398
Db 2242 CCTGTTTGTGCGGGGCTGAGACAGCTCACCAGTCAAGGACTTCTGAAAGCTGGGGAAGA 2301
Qy 2399 GAACATTTTTTAACGACAGACATTTTCCCTCTCTGTGTACCGAAGAGCCGCTGACAGATTCC 2458
Db 2302 GAACATTTTTTAACGACAGACATTTTCCCTCTCTGTGTACCGAAGAGCCGCTGACAGATTCC 2361
Qy 2459 AAGGAGCTTGTGCTACTGTGATCCATTCAGACCTGAGACAGATTAAGAAAGATGTGT 2518
Db 2362 AAGGAGCTTGTGCTACTGTGATCCATTCAGACCTGAGACAGATTAAGAAAGATGTGT 2421
Qy 2519 GACAGCAAGTACATCATCTCAGCTCTGTGATGAAGAAATCTCTGTGTGTGAGAGCTGT 2578
Db 2422 GACAGCAAGTACATCATCTCAGCTCTGTGATGAAGAAATCTCTGTGTGTGAGAGCTGT 2481

OY	2579	AGGATTCAGATGAAACTTGAATTTTTCCTCCAAAGGAAGTTCTGACATGCCACAGACAGT	2638
Db	2482	AGGATTCAGATGAAACTTGAATTTTTCCTCCAAAGGAAGTTCTGACATGCCACAGACAGT	2541
OY	2639	TGCTTCCCTGGATGGCAAAATGCTCCATCAGCTGATGATGATAGACTGTGAATTTCTTACCT	2698
Db	2542	TGCTTCCCTGGATGGCAAAATGCTCCATCAGCTGATGATGATAGACTGTGAATTTCTTACCT	2601
OY	2699	CATAGACAATTAATGATTTTATTTTGGTGTGGAAGACTACACACAGACTGGAGACTTTT	2758
Db	2602	CATAGACAATTAATGATTTTATTTTGGTGTGGAAGACTACACACAGACTGGAGACTTTT	2651
OY	2759	TGGGACATCGAGGAGACTGTGATGAACAAATTCCTAACAAATGGCGTCTTTAAAGAAT	2818
Db	2662	TGGGACATCGAGGAGACTGTGATGAACAAATTCCTAACAAATGGCGTCTTTAAAGAAT	2721
OY	2819	TACCTTTATGACTACCAAGCAGCATGTGTAGAGCCACACAGAAAGCAGCATGGCGGCCA	2878
Db	2722	TACCTTTATGACTACCAAGCAGCATGTGTAGAGCCACACAGAAAGCAGCATGGCGGCCA	2781
OY	2879	TGGCCTCTGGATCTTATTAATGCTTCCCTGTGCAGTAAATGATCATGACAGAACT	2938
Db	2782	TGGCCTCTGGATCTTATTAATGCTTCCCTGTGTGAGTAAATGATCATGACAGAACT	2841
OY	2939	TGTCTTGTTCCTGGTGGAAATTTAACTCTGACAGTTGGTGCACCTCGATATGACAGTAA	2998
Db	2842	TGTCTTGTTCCTGGTGGAAATTTAACTCTGACAGTTGGTGCACCTCGATATGACAGTAA	2901
OY	2999	AGCCCAAGAAATTTAAACAGACAGCCTGGAGCCTGTGATACATGAATATCCACATTCGCTGC	3058
Db	2902	AGCCCAAGAAATTTAAACAGACAGCCTGGAGCCTGTGATACATGAATATCCACATTCGCTGC	2961
OY	3059	TGAGCGCACCATCAAGGAGACTACAGGGAATATTGCTTGAAGACTGCTCCAAAGTCTT	3118
Db	2962	TGAGCGCACCATCAAGGAGACTACAGGGAATATTGCTTGAAGACTGCTCCAAAGTCTT	3021
OY	3119	TGTCAATCCAGCAAAATCCCAAGCAGCAACCTGTTCATGTGTGTGTGGACAGCAGTGGCT	3178
Db	3022	TGTCAATCCAGCAAAATCCCAAGCAGCAACCTGTTCATGTGTGTGTGGACAGCAGTGGCT	3081
OY	3179	CTGTGATCTGTGGCCCCCATCAACATGGCAGCCATTTGAATAGATTAATGAATCCCT	3238
Db	3082	CTGTGATCTGTGGCCCCCATCAACATGGCAGCCATTTGAATAGATTAATGAATCCCT	3141
OY	3239	TAAGTGTGAACGTCTAAAGGCCAGAAATACAGAAAGCGGCCAGAAATCTTGTATGGCTT	3298
Db	3142	TAAGTGTGAACGTCTAAAGGCCAGAAATACAGAAAGCGGCCAGAAATCTTGTATGGCTT	3201
OY	3299	CCATCCTGAGGAAATGCAAGGAGTGTGGGGTGGCCGAGTCTTCAAGCCAGACAGT	3358
Db	3202	CCATCCTGAGGAAATGCAAGGAGTGTGGGGTGGCCGAGTCTTCAAGCCAGACAGT	3261
OY	3359	CCCTCTTCTGACCCCTCTCTTTTGTATGCTCTTCTCAAGGTGACACTGTAGATGTTC	3418
Db	3262	CCCTCTTCTGACCCCTCTCTTTTGTATGCTCTTCTCAAGGTGACACTGTAGATGTTC	3321
OY	3419	TCTTACTGACTAGATTTTCTCTTGGCATGTAAATCATGATTAACACTGGAACCAAAAT	3478
Db	3322	TCTTACTGACTAGATTTTCTCTTGGCATGTAAATCATGATTAACACTGGAACCAAAAT	3381
OY	3479	ATGGGTGCAACATACGAGACATTAATATAGTCCAAACCATACGATCTCATCATGATTTTAA	3538
Db	3382	ATGGGTGCAACATACGAGACATTAATATAGTCCAAACCATACGATCTCATCATGATTTTAA	3441
OY	3539	ACTGTGCGTGAATATAACGCTTAAAGATATATGTGTGACAAAAGTTATCTATCATCTTTTAA	3598
Db	3442	ACTGTGCGTGAATATAACGCTTAAAGATATATGTGTGACAAAAGTTATCTATCATCTTTTAA	3501
OY	3599	CTTTTGCAGTCAATGATGATTTTGTGATTTTGCACATGATATATCACTTATCAAGAAATGGG	3658
Db	3502	CTTTTGCAGTCAATGATGATTTTGTGATTTTGCACATGATATATCACTTATCAAGAAATGGG	3561
OY	3659	ACCGAAGTGGTAGGCACTGTCCCTTCTGTGTAACCACTATTGAACCAATTTTAAACTG	3718

[illegible]

RESULT 5
AAA09261
ID AAA09261 standard; cDNA; 3598 BP.

AC AAAA09261;

DT 10-AUG-2000 (first entry)

Human alpha-2-delta-C gene splice variant.

KW alpha-2-delta-C; calcium channel subunit; 3p21.1; gabapentin; cyostatic;
KW anticonvulsant; antimigrane; antiparkinsonian; antidepressant;
KW

KW splice variant; ss.

OS Homo sapiens.

PN WO200020450-A2.

PD 13-APR-2000.

PF 07-OCT-1999; 99WO-US23519.

PR 07-OCT-1998; 98US-0103322.

PR 29-DEC-1998; 98US-0114088.

PA (WARN) WARNER LAMBERT CO.

PI Johns MA, Moldover B, Offord JD;

DR WPI; 2000-303744/26.

PT New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
PT proteins, useful in the treatment of epilepsy, migraine, chronic pain,
PT anxiety, multiple sclerosis or cancer

PS Claim 22; Page 85-86; 88pp; English.

CC The alpha-2-delta-C gene encodes a calcium channel subunit polypeptide.
CC
CC The alpha-2-delta-C gene is mapped to chromosome 3p21.1. This gene and the related
CC alpha-2-delta-D and -B genes are useful for protecting mammalian cells
CC from abnormal calcium flux by introducing expression vectors containing
CC the respective gene into mammalian cells. The antisense genes are also
CC useful for treating or preventing epilepsy. The alpha-delta-2-A protein
CC is a high-affinity binding target of the anti-convulsant drug gabapentin.
CC Therefore, alpha-delta-2 proteins may also be targeted to treat
CC seizure-related syndromes, migraine, ataxia, vestibular defects, chronic
CC pain, sleep interference, anxiety, amyotrophic lateral sclerosis (ALS),
CC multiple sclerosis, mania, tremor, parkinsonism, substance abuse or
CC addiction syndromes, mood, depression or cancer.

Sequence 3598 BP; 1004 A; 836 C; 904 G; 853 T; 1 other;

Query Match	90.28;	Score 3399.2;	DB 21;	Length 3598;
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Matches 3594; Conservative 0; Mismatches 4; Indels 172; Gaps 2;

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9Y 1 TACTATAGGCGCGCGAATTCGGCAGAGGCGCGCGAGCGGAGCAGCAGCCCCGC 60

61 GCGCTGCCACCGCCGCTCCGGCAGCTCCCCCGCGCCGCTCTGTCCGCCGCCGAGC 12

Db 61. GCGCTGCCACCGCCGCTCCGGCAGCTCCCGCGGCCGCTCTGTCGCCGCCGAC 12

QY	121	GGGCGCGTGGGAGGAGGCCACATGCGCCGGGCGGGCTCCGCCGCCGCCGCGTCCGGG	180
Db	121	GGGCGCGTGGGAGGAGGCCACATGCGCCGGGCGGGCTCCGCCGCCGCCGCGTCCGGG	180
QY	181	GGGCGCTGGCGCTTTCGCGTGGCGGCGCTTCTACGCCGGCGCTGGGGACGCTGGTGGCT	240
Db	181	GGGCGCTGGCGCTTTCGCGTGGCGGCGCTTCTACGCCGGCGCTGGGGACGCTGGTGGCT	240
QY	241	CGGAGCAGAGATACCGGCTCTCCGTTGTAAGCTCTGGGGCTCGGGCTTTTGGTGGGAGA	300
Db	241	CGGAGCAGAGATACCGGCTCTCCGTTGTAAGCTCTGGGGCTCGGGCTTTTGGTGGGAGA	300
QY	301	TAAATCCATTCTCTGCTAAGTACTCCGGTCTCCAGCTTCTGCAAAAGAAATACAAAGAT	360
Db	301	TAAATCCATTCTCTAAGTACTCCGGTCTCCAGCTTCTGCAAAAGAAATACAAAGAT	360
QY	361	ATGAGAAAGACCTTCCATAGAAAGAAATGTATGGCGTCCAACTGGTAAAGAGCTGGCAA	420
Db	361	ATGAGAAAGACCTTCCATAGAAAGAAATGTATGGCGTCCAACTGGTAAAGAGCTGGCAA	420
QY	421	AGAACATGGAAGATGTTTTCACAAAGATCTGAGGCCGTCAGCGCTCTGGTGGAGGCTG	480
Db	421	AGAACATGGAAGATGTTTTCACAAAGATCTGAGGCCGTCAGCGCTCTGGTGGAGGCTG	480
QY	481	CGAAGAGCGACCTCGTAAACATGAATTTGATGACACTTACAGTATGAATACTTCAATG	540
Db	481	CGAAGAGCGACCTCGTAAACATGAATTTGATGACACTTACAGTATGAATACTTCAATG	540
QY	541	CTGTCTGATTAATTAAGAGGACAAAGACGGGATTTTGGAGCGTGGGAAAGAAATTC	600
Db	541	CTGTCTGATTAATTAAGAGGACAAAGACGGGATTTTGGAGCGTGGGAAAGAAATTC	600
QY	601	TCTTAGCCCCCAATGACATTTTAAATATTTGCCCTGGAACATCAGTCTAAGGACGCTC	660
Db	601	TCTTAGCCCCCAATGACATTTTAAATATTTGCCCTGGAACATCAGTCTAAGGACGCTC	660
QY	661	AGTACCCAAGCAACATGTACACAAAGACCCCTGCAATTTGTCAATGGGGTTATTTGGTCTG	720
Db	661	AGTACCCAAGCAACATGTACACAAAGACCCCTGCAATTTGTCAATGGGGTTATTTGGTCTG	720
QY	721	AATCTCTAAACAAAGTTTCTTGTAGATTAATCTTGTGACCGTGCACATCCTATTTGGCACT	780
Db	721	AATCTCTAAACAAAGTTTCTTGTAGATTAATCTTGTGACCGTGCACATCCTATTTGGCACT	780
QY	781	ACTTTGGAATGTCAAAGGGCTTTTATAGGCAAGTATCCGGGGATTTAAATGCGACAGATG	840
Db	781	ACTTTGGAATGTCAAAGGGCTTTTATAGGCAAGTATCCGGGGATTTAAATGCGACAGATG	840
QY	841	AGATAGGAGTATGTCCTTGACGTGACGAGAACCGAAATGTATCATCCAGCAACTT	900
Db	841	AGATAGGAGTATGTCCTTGACGTGACGAGAACCGAAATGTATCATCCAGCAACTT	900
QY	901	CTCCGAAAGACGTGGTCAATTTTATGTTAGCTGAGCTGAGAGCAATGACGCTCTGA	960
Db	901	CTCCGAAAGACGTGGTCAATTTTATGTTAGCTGAGCTGAGAGCAATGACGCTCTGA	960
QY	961	CTATTCGGAAGCAAAAGCTCATCTCATCTTTTGGATACACTTTGGGGATGTATGACTTCTCA	1020
Db	961	CTATTCGGAAGCAAAAGCTCATCTCATCTTTTGGATACACTTTGGGGATGTATGACTTCTCA	1020
QY	1021	ACATTAATTTGCTTATTAATGAGGAGCTTCACTATGTGAAACCTTGGCGAATGGAACCTTTGG	1080
Db	1021	ACATTAATTTGCTTATTAATGAGGAGCTTCACTATGTGAAACCTTGGCGAATGGAACCTTTGG	1080
QY	1081	TGCAGCGCAGAGACCAAAAGAGACACTTCAGGGAGATCTGGACAAATCTTTTCGCA	1140
Db	1081	TGCAGCGCAGAGACCAAAAGAGACACTTCAGGGAGATCTGGACAAATCTTTTCGCA	1140
QY	1141	AAGGAATTTGAATGTTGGATTAAGCTGTGATATGAGGCTTCAACAATTCATATGATTTTCA	1200
Db	1141	AAGGAATTTGAATGTTGGATTAAGCTGTGATATGAGGCTTCAACAATTCATATGATTTTCA	1200
QY	1201	ACGACAGGGGACAAAGATATGTGCAATCAGGCCATCATCTCTCAATACATGATGGGGCGG	1260

Db	1201	ACACACGGGACAAAGAAAGTATCTGCATCGACGCGCCATCATGCTCAAACTGATGGGGGG	1260
Qy	1261	TGGACACCTATGATTCACATCTTTTGGAAAATACAAATTTGGCCAGATGGAAGGTTGCATCT	1320
Db	1261	TGGACACCTATGATTCACATCTTTTGGAAAATACAAATTTGGCCAGATGGAAGGTTGCCATCT	1322
Qy	1321	TCACATACCTCAATTTGGACGAGAGGCTGGCTTTGGACACAATCTAAAGTGATGGCTGTG	1380
Db	1321	TCACATACCTCAATTTGGACGAGAGGCTGGCTTTGGACACAATCTAAAGTGATGGCTGTG	1380
Qy	1381	CCAAACAAAGGATTTTTTACCAGATCTCCACCTTGGCTGATGTGAGAGAAATGTCATGG	1440
Db	1381	CCAAACAAAGGATTTTTTACCAGATCTCCACCTTGGCTGATGTGAGAGAAATGTCATGG	1440
Qy	1441	AATACCTTCACGCTGTTATGACCGGCCCAAAGTCATCGACACAGAGATGATGTGGTGGA	1500
Db	1441	AATACCTTCACGCTGTTATGACCGGCCCAAAGTCATCGACACAGAGATGATGTGGTGGA	1500
Qy	1501	CCGAAGCTTACATTGACAGCAGCTGATGATGATCAAGGGCCCGCTCGATGACCACTG	1560
Db	1501	CCGAAGCTTACATTGACAGCAGCTGATGATGATCAAGGGCCCGCTCGATGACCACTG	1560
Qy	1561	TAGCCATGCTCTGTATTATGATAGCAGAAAGAACCAAGATCGAAGGGCATCTTCTGGGAG	1620
Db	1561	TAGCCATGCTCTGTATTATGATAGCAGAAAGAACCAAGATCGAAGGGCATCTTCTGGGAG	1620
Qy	1621	TGGTTGGACAGATGTCCCACTGTAAGAAACCTTGGAAGCCATCCCAAAATCAAGTTAG	1680
Db	1621	TGGTTGGACAGATGTCCCACTGTAAGAAACCTTGGAAGCCATCCCAAAATCAAGTTAG	1680
Qy	1681	GGATTTCACGGTTATGACCTTTGTCATTCACAAATATATGATATCTCGACGATCCGGAC	1740
Db	1681	GGATTTCACGGTTATGACCTTTGTCATTCACAAATATATGATATCTCGACGATCCGGAC	1740
Qy	1741	TCAGGCTGCTGTCAGGAAGAAAGAAAAAGCGAAGAAACCTAATATATGATGCTTGACC	1800
Db	1741	TCAGGCTGCTGTCAGGAAGAAAGAAAAAGCGAAGAAACCTAATATATGATGCTTGACC	1800
Qy	1801	TCCTCTGAGGTGGAGTGGGAAGACCGCAATATACGCTTTGAGAAATGCTATGTCATGAA	1860
Db	1801	TCCTCTGAGGTGGAGTGGGAAGACCGCAATATACGCTTTGAGAAATGCTATGTCATGAA	1860
Qy	1861	AGACGGGGAAGTTTCCATGAGAGTGAAGAAGACAGTGGCAAAAGGGAACCGGTTTTGG	1920
Db	1861	AGACGGGGAAGTTTCCATGAGAGTGAAGAAGACAGTGGCAAAAGGGAACCGGTTTTGG	1920
Qy	1921	TGATGACAAATGACTACTATTATACAGACATCAAGGGTACTCTCTTCACTTATGATGTGG	1980
Db	1921	TGATGACAAATGACTACTATTATACAGACATCAAGGGTACTCTCTTCACTTATGATGTGG	1980
Qy	1981	CGCTTTCAGAGAGTCAATGGGAAATATTTCTTCGAGGGAATGTACACCATCGAAGAGCC	2040
Db	1981	CGCTTTCAGAGAGTCAATGGGAAATATTTCTTCGAGGGAATGTACACCATCGAAGAGCC	2040
Qy	2041	TGCTATGACTTAGAACAATCCGATGTGTCCTTGGCAGATGATGTGCTTACTGCAACACTG	2100
Db	2041	TGCTATGACTTAGAACAATCCGATGTGTCCTTGGCAGATGATGTGCTTACTGCAACACTG	2100
Qy	2101	ACCTACACCTTGAGCACCGCATCTGCTCAGTTAGAAAGGATTTAAGCTCTACTCTAAAG	2160
Db	2101	ACCTACACCTTGAGCACCGCATCTGCTCAGTTAGAAAGGATTTAAGCTCTACTCTAAAG	2160
Qy	2161	GCAGAAACCTCTGCTCCAGTGTGATTAAGAAATGTATCCAAAGAGTCCTTTTGAAGCGG	2220
Db	2161	GCAGAAACCTCTGCTCCAGTGTGATTAAGAAATGTATCCAAAGAGTCCTTTTGAAGCGG	2220
Qy	2221	TGGTGATGCTCCCATTTGAAGGATTTGGACACCGCTGGCCCTCAACAATCTGAAAAAT	2280
Db	2221	TGGTGATGCTCCCATTTGAAGGATTTGGACACCGCTGGCCCTCAACAATCTGAAAAAT	2280
Qy	2281	CTGACAAAGGCTGAGATTTGCTTCTTGAGACTGACAGGGGCTCTCAGAAATCAAC	2340
Db	2281	CTGACAAAGGCTGAGATTTGCTTCTTGAGACTGACAGGGGCTCTCAGAAATCAAC	2340

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Db 2281 CTGACAAAGGCGGTGAGGTTCTCTCTCGGACCTGCGACGCGGCTCTCCAGAAATCAACC 2340
Oy 2341 TGTGTTGCGGGGCTGAGCAGCTCAGCAATCGAGCTTCTGTAAGCTGGGCAAGAGGA 2400
Db 2341 TGTGTTGCGGGGCTGAGCAGCTCAGCAATCGAGCTTCTGTAAGCTGGGCAAGAGGA 2400
Oy 2401 ACATTTTAAACGACAGCAATTTTCCCTCTCTGTGTACCGAAGAGCCGCTGAGAGATTTCCAG 2460
Db 2401 ACATTTTAAACGACAGCAATTTTCCCTCTCTGTGTACCGAAGAGCCGCTGAGAGATTTCCAG 2460
Oy 2461 GGAGCTCTGCTACTGATCCCATTCAGACACTGACAGCACTGATTAAGCAATGTGGTGA 2520
Db 2461 GGAGCTCTGCTACTGATCCCATTCAGACACTGACAGCACTGATTAAGCAATGTGGTGA 2520
Oy 2521 CAGCAATACATCCATCAGCTCTGCTGATGAAGCAATCTCTGTGGTGGCAGCTGTAG 2580
Db 2521 CAGCAATACATCCATCAGCTCTGCTGATGAAGCAATCTCTGTGGTGGCAGCTGTAG 2580
Oy 2581 GCATTCAGATGAATCTGAATTTTTCAGAAAGGATTTCTGAGCTGCGACAGACAGTGTG 2640
Db 2581 GCATTCAGATGAATCTGAATTTTTCAGAAAGGATTTCTGAGCTGCGACAGACAGTGTG 2640
Oy 2641 CTTCCTGATGAGCAATGCTCTGCTGACGCTGTGATGATGAGACTGTGAATTTGTTACTCA 2700
Db 2641 CTTCCTGATGAGCAATGCTCTGCTGACGCTGTGATGATGAGACTGTGAATTTGTTACTCA 2700
Oy 2701 TAGCAATTAATGATTAATTTTGGTGTCTGAMAGCTACACAGACAGTGGAGCTTTTGG 2760
Db 2680 -----AGACTGGAGACTTTTGG 2697
Oy 2761 GTGAGATCGAGGAGCTGTGATGAACAAATGCTAACAAATGGGCTCTTTAAAGAAATTA 2820
Db 2698 GTGAGATCGAGGAGCTGTGATGAACAAATGCTAACAAATGGGCTCTTTAAAGAAATTA 2757
Oy 2821 CCGTTATGACTACCAAGCCATGTGTAGAGCAACAGAAAGAGCAGGATGGCCCATG 2880
Db 2758 CCGTTATGACTACCAAGCCATGTGTAGAGCAACAGAAAGAGCAGGATGGCCCATG 2817
Oy 2881 GCCTCTGATGCTTATTAATGCTCTCTCTGACAGTAATGATGATGACAGAACTTG 2940
Db 2818 GCCTCTGATG----- 2828
Oy 2941 TCTTGTCTCTGCTGTAATTTAACCTCTGCAAGTTGGTGGACCTCGATATGACAGCTAAG 3000
Db 2829 ----- 2828
Oy 3001 CCCAGAAATTTGAACAGACCCCTGAGCTGTGTATCTGAATATCCAGCATTTGCTCTCG 3060
Db 2829 CCCAGAAATTTGAACAGACCCCTGAGCTGTGTATCTGAATATCCAGCATTTGCTCTCG 2888
Oy 3061 AGGCGACCATCAAGAGAGACTACAGGAAATATTGCTGTGAAGACTGCTCCAGTCTCTTG 3120
Db 2889 AGGCGACCATCAAGAGAGACTACAGGAAATATTGCTGTGAAGACTGCTCCAGTCTCTTG 2948
Oy 3121 TCATCCAGCAATCCCAAGCAGCAACCTGTTCATGTTGTTGTTGAGCAGACAGCTGCTCT 3180
Db 2949 TCATCCAGCAATCCCAAGCAGCAACCTGTTCATGTTGTTGTTGAGCAGCAACCTGCTCT 3008
Oy 3181 GTGAATCTGTGGCCCCCATCAGCATGGCAACCATTAATCAAGTATTAATGATCCCTTA 3240
Db 3009 GTGAATCTGTGGCCCCCATCAGCATGGCAACCATTAATGATTAATGATCCCTTA 3068
Oy 3241 AGTGTGAACGTCTAAAGGCCAGAAAGATCAGAAAGGCCAGAAATCTTCATGGCTTCC 3300
Db 3069 AGTGTGAACGTCTAAAGGCCAGAAAGATCAGAAAGGCCAGAAATCTTCATGGCTTCC 3128
Oy 3301 ATCTGAGAGAAATCGAAGGAGTGTGGGGGTGCGCCGAGTCTCCAAAGCCAGACAGTCC 3360
Db 3129 ATCTGAGAGAAATCGAAGGAGTGTGGGGGTGCGCCGAGTCTCCAAAGCCAGACAGTCC 3188
Oy 3361 TCCCTCTGCTCTGCTGCTTTGATGCTCTTCTCAAGGTGACAGCTGATGAGATGTTCTC 3420
Db 3189 TCCCTCTGCTCTGCTGCTTTGATGCTCTTCTCAAGGTGACAGCTGATGAGATGTTCTC 3248

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Oy 3421 TTAGCACTGAGATGTTCTCTTGGCATGCTAAATCATGATGAATAACTGGAACCAAAATAT 3480
Db 3249 TTAGCACTGAGATGTTCTCTTGGCATGCTAAATCATGATGAATAACTGGAACCAAAATAT 3308
Oy 3481 GGTGCAACATATCGAGACATGAAATATAGTCGAACCATCAGCATCTCATCATGATTTTAAAC 3540
Db 3309 GGTGCAACATATCGAGACATGAAATATAGTCGAACCATCAGCATCTCATCATGATTTTAAAC 3368
Oy 3541 TGTGCGTGATTAATTAACCTTTAAAGATATGTTGACAAAAAGTTATCTATCATCTTTTACT 3600
Db 3369 TGTGCGTGATTAATTAACCTTTAAAGATATGTTGACAAAAAGTTATCTATCATCTTTTACT 3428
Oy 3601 TTTGCGCATGCAAAATGTGATTTGGCACATGATTAATCAACCTTCATCAGAAATGGGAC 3660
Db 3429 TTTGCGCATGCAAAATGTGATTTGGCACATGATTAATCAACCTTCATCAGAAATGGGAC 3488
Oy 3661 CGCAAGTGTAGCAGCTGCTCTCTGCTGCAACCTATTGAACCAATTTAAACGTG 3720
Db 3489 CGCAAGTGTAGCAGCTGCTCTCTGCTGCAACCTATTGAACCAATTTAAACGTG 3548
Oy 3721 TACTTTTAAATTAAGTATTAATTAATCAATTAATTAATTAATTAATTAATTAATTAAT 3770
Db 3549 TACTTTTAAATTAAGTATTAATTAATCAATTAATTAATTAATTAATTAATTAATTAAT 3598

RESULT 6
AA01409
ID AA01409 standard; cDNA; 3213 BP.
XX
AC AA01409;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human secreted soluble alpha2delta calcium channel subunit #6 cDNA.
XX
KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
KW filter binding assay; wheat germ lectin flashplate assay; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..3213
FT /tag= a
FT /product= "Alpha2delta calcium channel subunit #6"
FT /note= "This sequence lacks a stop codon."
FT /transl_except= (pos:3130..3153,aa:Arg-Arg)
FT /note= "These two codons between them have an
FT apparent 18 nucleotide insertion"
XX
PN WO200119870-A2.
XX
PD 22-MAR-2001.
XX
PE 18-SEP-2000; 2000WO-EP09137.
XX
PR 16-SEP-1999; 99US-0397550.
XX
PA (WARN ) WARNER LAMBERT CO.
XX
PI Brown JP, Bertelli F;
XX
DR WPI; 2001-235262/24.
DR P-PSDB; AAU01019.
XX
PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or
PT Wheat germ lectin Flashplate assays -
XX
PS Claim 39; Page 71-72; 16pp; English.

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1944 ACAGACATCAAGGGTACTCCTTTCAGTTAGTGTGGCGCTTTCAGAGTCATGGGAAA 2003
1801 ACAGACATCAAGGGTACTCCTTTCAGTTAGTGTGGCGCTTTCAGAGTCATGGGAAA 1860
2004 TATTTCTTCGAGGGAATGTAAACCATGGAAGAGCCCTGCATGACTTAAACATCCGAT 2063
1861 TATTTCTTCGAGGGAATGTAAACCATGGAAGAGCCCTGCATGACTTAAACATCCGAT 1920
2064 GTGTCTTCGAGGGAATGTAAACCATGGAAGAGCCCTGCATGACTTAAACATCCGAT 2123
1921 GTGTCTTCGAGGGAATGTAAACCATGGAAGAGCCCTGCATGACTTAAACATCCGAT 1980
2124 CTGTCTTCGAGGGAATGTAAACCATGGAAGAGCCCTGCATGACTTAAACATCCGAT 2183
1981 CTGTCTTCGAGGGAATGTAAACCATGGAAGAGCCCTGCATGACTTAAACATCCGAT 2040
2184 GATTAAGCAATTTGATCCAAAGAGTCTTTTTCAGCGCGGTGGTGAAGTCCCATTTGAAGCG 2243
2041 GATTAAGCAATTTGATCCAAAGAGTCTTTTTCAGCGCGGTGGTGAAGTCCCATTTGAAGCG 2100
2244 TATTTGACACAGCTGGCGCTTCACAAATCTGAAATTTCTGACAAAGGCGGTGGAGTTGCC 2303
2101 TATTTGACACAGCTGGCGCTTCACAAATCTGAAATTTCTGACAAAGGCGGTGGAGTTGCC 2160
2304 TTTCTGCGACACTGCGACAGGCGCTCTCCAGAAATCACTGTTTTCGCGGCGCTGACAGACTC 2363
2161 TTTCTGCGACACTGCGACAGGCGCTCTCCAGAAATCACTGTTTTCGCGGCGCTGACAGACTC 2220
2364 ACCAATCAGACACTTCTGAAAGCTGGCGACAGAGAACATTTTTCAGCAGACATTTTC 2423
2221 ACCAATCAGACACTTCTGAAAGCTGGCGACAGAGAACATTTTTCAGCAGACATTTTC 2280
2424 CCTCTCTGACAGGAGAGGCGCTGACAGAGATTCACAGAGCTTCTGTAAGTCCATCCCA 2483
2281 CCTCTCTGACAGGAGAGGCGCTGACAGAGATTCACAGAGCTTCTGTAAGTCCATCCCA 2340
2484 TTTGAGCAGTGGACAGTCAATTAAGCAATGTGTGACAGCAGTCAATCCATCCAGCTTC 2543
2341 TTTGAGCAGTGGACAGTCAATTAAGCAATGTGTGACAGCAGTCAATCCATCCAGCTTC 2400
2544 CTGGATGAACGGAATCTCTGTGTGGGAGCTGTAGGCAATTCAGATGAACATTTGAATTT 2603
2401 CTGGATGAACGGAATCTCTGTGTGGGAGCTGTAGGCAATTCAGATGAACATTTGAATTT 2460
2604 TTTCCAAAGGAAGTTCTGACACTGCGACAGACAGTGTCTTCCCTGATGGCAATGCTCC 2663
2461 TTTCCAAAGGAAGTTCTGACACTGCGACAGACAGTGTCTTCCCTGATGGCAATGCTCC 2520
2664 ATCAGCTGTGATGATGAGACTGTGAATTTTACCTCATAGCAATTAATGATTTATTTTG 2723
2521 ATCAGCTGTGATGATGAGACTGTGAATTTTACCTCATAGCAATTAATGATTTATTTTG 2580
2724 GTGTCTGAAGACTACACAGACTGAGACTTTTGTGTGAGATCGAGGAGCTGTGATG 2783
2581 GTGTCTGAAGACTACACAGACTGAGACTTTTGTGTGAGATCGAGGAGCTGTGATG 2640
2784 AACCAATTTGCTAAACATGGGCTCTTTTAAACAAATTTACCTTTATGACTACCAAGCCATG 2843
2641 AACCAATTTGCTAAACATGGGCTCTTTTAAACAAATTTACCTTTATGACTACCAAGCCATG 2700
2844 TGTAGAGCCAAACAGAAAGCAGCATGGCGCCCATGCTCTGATTCCTTATATATGCG 2903
2701 TGTAGAGCCAAACAGAAAGCAGCATGGCGCCCATGCTCTGATTCCTTATATATGCG 2760
2904 TTTCTCTCTGAGTAAATGATGATGACAGAACTTGTCTTCTGCTGTGGAATTTAAC 2963
2761 TTTCTCTCTGAGTAAATGATGATGACAGAACTTGTCTTCTGCTGTGGAATTTAAC 2820
2964 CTCTCTCATTTGGTGGCACTCCGATATGACAGCTTAAAGCCCAAAATTTGAACAGACCCCTG 3023
2821 CTCTCTCATTTGGTGGCACTCCGATATGACAGCTTAAAGCCCAAAATTTGAACAGACCCCTG 2880

3024 GAGCCTTGTGATGATGATATCCAGCATTTGCTCTGACGCGCACCATTCAGAGACTTACA 3083
2881 GAGCCTTGTGATGATGATATCCAGCATTTGCTCTGACGCGCACCATTCAGAGACTTACA 2940
3084 GCGAATATTGCTTGTGAAGACTGCTCAAGTCTTTTTCATCCAGCAATTCGCAAGGAGC 3143
2941 GCGAATATTGCTTGTGAAGACTGCTCAAGTCTTTTTCATCCAGCAATTCGCAAGGAGC 3000
3144 AACCTTTATGCTGTGTGTGAGCAGAGCTGCTCTGTGAATCTGTGGCCCCCATACC 3203
3001 AACCTTTATGCTGTGTGTGAGCAGAGCTGCTCTGTGAATCTGTGGCCCCCATACC 3060
3204 ATGGCACCATTGAAATCAGATTAATGATTCCTTAAAGTGTAGAGTCTTAAA----- 3256
3061 ATGGCACCATTGAAATCAGATTAATGATTCCTTAAAGTGTAGAGTCTTAAAGGCCCCAG 3120
3257 -----GGCCCCAGATCAGAAAGCGCCACAGATCTTGTGATGAGCTTCAATCCT 3305
3121 AAGATCAGAAAGGCGCCAGAAATCAGAAAGCGCCACAGATCTTGTGATGAGCTTCAATCCT 3180
3306 GAGGAGAAATCAGAAAGGAGTGTGGGGGTGCGCG 3338
3181 GAGGAGAAATCAGAAAGGAGTGTGGGGGTGCGCG 3213
RESULT 7
AAFS7546
ID AAF57546 standard; DNA: 3213 BP.
XX
XX AAF57546:
XX
DT 11-JUN-2001 (first entry)
XX
XX Human calcium channel alpha2delta subunit encoding DNA.
DE
XX
XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
KW nervous system disorder; pain; epilepsy; anxiety; human; ds.
OS
XX Homo sapiens.
OS
PN W0200120336-A2.
XX
PD 22-MAR-2001.
XX
PE 18-SEP-2000; 2000MO-EP09136.
XX
PR 16-SEP-1999; 99US-0397549.
XX
PA (WARN) WARNER LAMBERT CO.
XX
XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;
PI WPI: 2001-257902/26.
DR P-PSDB: AAB62243.
XX
PT Competitive binding assay for screening ligands which bind a cerebral
PT cortical voltage-dependent calcium channel alpha2-delta-1 subunit,
PT where the ligands identified are useful for treating disorders of the
PT nervous system, including pain -
XX
XX
PS Disclosure: Page 71-72; 158pp; English.
XX
XX The invention relates to a new method for screening ligands which bind a
CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
CC preferably alpha2delta-1 subunit. The method comprises contacting a
CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of
CC interest and a labelled compound which binds the subunit, followed by
CC measuring the level of binding of the labelled compound to alpha2delta-1
CC subunit. The method is useful for screening ligands, preferably
CC biologically active products that modulate a nervous system function,
CC which bind a cerebral cortical voltage-dependent calcium channel
CC alpha2delta-1 subunit. The ligands identified by the method are useful
CC for treating disorders of the nervous system, including pain, epilepsy

CC and anxiety. The present sequence represents a human calcium channel
CC alpha2delta subunit encoding DNA.

XX Sequence 3213 BP; 894 A; 727 C; 824 G; 767 T; 1 other;

Query Match 84.0%; Score 3166.6; DB 22; Length 3213;
Best Local Similarity 99.4%; Pired. No. 0;
Matches 3195; Conservative 0; Mismatches 0; Indels 18; Gaps 1;

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QY 144 ATGCGCGGGCGGGCTGCGCGCGCGCGCGCTCCGGGGGGCGCTCGCGCGCTTCGCGCGCC 203
    |||||
Db 1 ATGCGCGGGCGGGCTGCGCGCGCGCGCGCTCCGGGGGGCGCTCGCGCGCTTCGCGCGCC 60
QY 204 GCGCTTCTCTAGCGCGCGCTGCGGGGACGTGTCGCTCGGAGCAGCAGATACCGCTCTCC 263
    |||||
Db 61 GCGCTTCTCTAGCGCGCGCTGCGGGGACGTGTCGCTCGGAGCAGCAGATACCGCTCTCC 120
QY 264 GTGGTAGAGCTGTGGGCGCTCGCGCTTTGGTGGGAGATAAATCCATTCGCTGAAGTAC 323
    |||||
Db 121 GTGGTAGAGCTGTGGGCGCTCGCGCTTTGGTGGGAGATAAATCCATTCGCTGAAGTAC 180
QY 324 TCCGCTTCCAGCTTCTGCAAAAGAAATACAAAGATGAGAGAAAGCGTTGCCATAGAA 383
    |||||
Db 181 TCCGCTTCCAGCTTCTGCAAAAGAAATACAAAGATGAGAGAAAGCGTTGCCATAGAA 240
QY 384 GAAATGATGCGCTCCACTGTGTAAGAAAGCTGGCAAAACATGGAAGAGATGTTTAC 443
    |||||
Db 241 GAAATGATGCGCTCCACTGTGTAAGAAAGCTGGCAAAACATGGAAGAGATGTTTAC 300
QY 444 AAGAAGTCTGAGGCGCTGACGCGCTCTGTGTGAGAGCTGCAAGAAACACCTGAAACAT 503
    |||||
Db 301 AAGAAGTCTGAGGCGCTGACGCGCTCTGTGTGAGAGCTGCAAGAAACACCTGAAACAT 360
QY 504 GAATTTGATGCACTTACAGTATGAATCTCAATGCTGCTGTGTAATGAAAGGAC 563
    |||||
Db 361 GAATTTGATGCACTTACAGTATGAATCTCAATGCTGCTGTGTAATGAAAGGAC 420
QY 564 AAAGACGGGAATTTTGGAGCTGGGAAAGAAATTCATCTAGCCCAATGACATTTT 623
    |||||
Db 421 AAAGACGGGAATTTTGGAGCTGGGAAAGAAATTCATCTAGCCCAATGACATTTT 480
QY 624 AATTAATTTGCCGTGTGAACATCACTAGTGAAGCTGTCACCAAGACATGTATCAAC 683
    |||||
Db 481 AATTAATTTGCCGTGTGAACATCACTAGTGAAGCTGTCACCAAGACATGTATCAAC 540
QY 684 AAAGACCTGCAATTTGTCAATGGGTTTATGGTCTGAATCTCTAAACAAGTTTTTGA 743
    |||||
Db 541 AAAGACCTGCAATTTGTCAATGGGTTTATGGTCTGAATCTCTAAACAAGTTTTTGA 600
QY 744 GATAACTTTGACCGTGAACCATCTCTCATATGCGAGTACTTTGGAAGTG 780
    |||||
Db 601 GATAACTTTGACCGTGAACCATCTCTCATATGCGAGTACTTTGGAAGTG 660
QY 804 TTTAGGCGAGTATCCGGGGATTAATGGAACCATGATGAAGTGAAGTCAATGCTTTCAC 863
    |||||
Db 661 TTTAGGCGAGTATCCGGGGATTAATGGAACCATGATGAAGTGAAGTCAATGCTTTCAC 720
QY 864 TGCAGAACCCGAAATGTATACATCCAGCAGCAATTTCTCCGAAAGAGTGCTCATTTTA 923
    |||||
Db 721 TGCAGAACCCGAAATGTATACATCCAGCAGCAATTTCTCCGAAAGAGTGCTCATTTTA 780
QY 924 GTTGACGTCACTGCGAGCATGAAGAGACTCGCTGACTATGCGAGACAAACATCTCA 983
    |||||
Db 781 GTTGACGTCACTGCGAGCATGAAGAGACTCGCTGACTATGCGAGACAAACATCTCA 840
QY 984 TCCATTTTGGATACACTTTGGGATGATGACTTTTCAACATATTTGCTTAAATAGAGAG 1043
    |||||
Db 841 TCCATTTTGGATACACTTTGGGATGATGACTTTTCAACATATTTGCTTAAATAGAGAG 900
QY 1044 CTTCACATATGTGAACCTTGCTGTAATGGAAGTGTGCAAGCGACAGCAAGCAAA 1103
    |||||
Db 901 CTTCACATATGTGAACCTTGCTGTAATGGAAGTGTGCAAGCGACAGCAAGCAAA 960
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QY 1104 GAGCATTTCAGGAGCATCTGACAAACTTTTGGCCAAAGAAATTTGGATTTGATATA 1163
    |||||
Db 961 GAGCATTTCAGGAGCATCTGACAAACTTTTGGCCAAAGAAATTTGGATTTGATATA 1020
QY 1164 GCTTCGTAATGAGGCGCTTCAACATTTGAGTGTATTTCAACACAGCGGACAAGAGTATC 1223
    |||||
Db 1021 GCTTCGTAATGAGGCGCTTCAACATTTGAGTGTATTTCAACACAGCGGACAAGAGTATC 1080
QY 1224 TGCAGTAGGCGCATATGCTCATTAATGATGAGGCGGTGACACCTATATGATACATCTT 1283
    |||||
Db 1081 TGCAGTAGGCGCATATGCTCATTAATGATGAGGCGGTGACACCTATATGATACATCTT 1140
QY 1284 GCAAAATATACATTTGGCCAGATTCGAAAGGTTGGCATCTTCAATACCTATGAGACGAG 1343
    |||||
Db 1141 GCAAAATATACATTTGGCCAGATTCGAAAGGTTGGCATCTTCAATACCTATGAGACGAG 1200
QY 1344 GCTGCGTTTGCAGACAAATCTAAAGTGATGCGCTGTCGCAACAAAGATTTTACCAG 1403
    |||||
Db 1201 GCTGCGTTTGCAGACAAATCTAAAGTGATGCGCTGTCGCAACAAAGATTTTACCAG 1260
QY 1404 ATCTCCACCTTGGCTGATGTGTCAGAGAAATGTATGCAATACCTTACGCTTACCGG 1463
    |||||
Db 1261 ATCTCCACCTTGGCTGATGTGTCAGAGAAATGTATGCAATACCTTACGCTTACCGG 1320
QY 1464 CCCAAAGTCATGACACGAGGAGCATGATGATGATGAGCGGACCGAACCCTTACATGACACT 1523
    |||||
Db 1321 CCCAAAGTCATGACACGAGGAGCATGATGATGATGAGCGGACCGAACCCTTACATGACACT 1380
QY 1524 CTGACTGATGATGAGGCGCGCTGCTGATGACACTGTATGACCTGCTGCTGTTTAAAG 1583
    |||||
Db 1381 CTGACTGATGATGAGGCGCGCGCTGCTGATGACACTGTATGACCTGCTGCTGTTTAAAG 1440
QY 1584 CAGAACGAAACAGATGCAAGGAGGCTTCTGGAAGTGTGAGGAGCAGATGTCCAGTG 1643
    |||||
Db 1441 CAGAACGAAACAGATGCAAGGAGGCTTCTGGAAGTGTGAGGAGCAGATGTCCAGTG 1500
QY 1644 AAAGACTTCTGAGAACCATCCCCCAATACAAATGATGAGGATTCACGCTTATGCTTGA 1703
    |||||
Db 1501 AAAGACTTCTGAGAACCATCCCCCAATACAAATGATGAGGATTCACGCTTATGCTTGA 1560
QY 1704 ATCCAAATATGATGATATTCCTGAGCAGATCCGGAATAGGCTGTGATGCAAGAGGA 1763
    |||||
Db 1561 ATCCAAATATGATGATATTCCTGAGCAGATCCGGAATAGGCTGTGATGCAAGAGGA 1620
QY 1764 AAAAAGCGAAGAACTTACTATAGTACGCTTGAACCTCTCTGAGGTGAGAGTGGAGAAC 1823
    |||||
Db 1621 AAAAAGCGAAGAACTTACTATAGTACGCTTGAACCTCTCTGAGGTGAGAGTGGAGAAC 1680
QY 1824 CGAGATGAGCTGTGAGAAATGCTATGTTGAATCGAAGAGCGGGAAGTTTCCATGAG 1883
    |||||
Db 1681 CGAGATGAGCTGTGAGAAATGCTATGTTGAATCGAAGAGCGGGAAGTTTCCATGAG 1740
QY 1884 GTGAAGAGACAGTGTGACAAAGGGAAGCGTTTGGTGTATGACAAATGATACATATAT 1943
    |||||
Db 1741 GTGAAGAGACAGTGTGACAAAGGGAAGCGTTTGGTGTATGACAAATGATACATATAT 1800
QY 1944 ACAGACATCAAGGATACCTCTTCACTTGTAGTGTGCGCTTCCAGAGTATGGGAAA 2003
    |||||
Db 1801 ACAGACATCAAGGATACCTCTTCACTTGTAGTGTGCGCTTCCAGAGTATGGGAAA 1860
QY 2004 TATTTCTTCCGAGGAAATGTAACATGCAAGAGCGCTGACATGACTTGAACATCCGAT 2063
    |||||
Db 1861 TATTTCTTCCGAGGAAATGTAACATGCAAGAGCGCTGACATGACTTGAACATCCGAT 1920
QY 2064 GTGTCCTTGGCAGATGATGCTCTACGCAACATGACCTAATACCTGACACCGCCAT 2123
    |||||
Db 1921 GTGTCCTTGGCAGATGATGCTCTACGCAACATGACCTAATACCTGACACCGCCAT 1980
QY 2124 CTGCTCAGTTAGAAAGCATTAAGCTTACCTAAAGGCAAGAAACCTCTCTCAGAGT 2183
    |||||
Db 1981 CTGCTCAGTTAGAAAGCATTAAGCTTACCTAAAGGCAAGAAACCTCTCTCAGAGT 2040
QY 2184 GATTAAGAAATGATCCAAAGAGTCTTTTGAACGCGGTGTGAGTGCCTCCATTGAAGCG 2243
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Db 2041 GATAAAGATTGATCAAGAGTCTTTTTCAGCGGGTGTGAGTGGCCCATTTAAACG 2100
Oy 2244 TATTGGACACCTGGCCCTCAACAAATCTGAAAATTTTGACAGAGCGCTGAGGTTGCC 2303
Db 2101 TATTGGACACCTGGCCCTCAACAAATCTGAAAATTTTGACAGAGCGCTGAGGTTGCC 2160
Oy 2304 TTCTCGGCACTGCGACGCGCTCTCCAGATTCAAACCTGTTGTGCGGGCTGAGACGCTC 2363
Db 2161 TTCTCGGCACTGCGACGCGCTCTCCAGATTCAAACCTGTTGTGCGGGCTGAGACGCTC 2220
Oy 2364 ACATATGAGACTTCTGAAAAGCTGGCGACAAGAGAAATTTTAAACGACCATTTTC 2423
Db 2221 ACCAATCAGACTCTCTGAAAAGCTGGCGACAAGAGAAATTTTAAACGACCATTTTC 2280
Oy 2424 CCCTCTGTTGATCCGAAAGCGCTGACAGATTTCCAGGAGCTTCTCTACTCATCCCA 2483
Db 2281 CCCTCTGTTGATCCGAAAGCGCTGACAGATTTCCAGGAGCTTCTCTACTCATCCCA 2340
Oy 2484 TTGACACTGACCAAGTCAATAAAGCAATGTGTGACAGCAATGATCATCCATCCAGCTC 2543
Db 2341 TTGACACTGACCAAGTCAATAAAGCAATGTGTGACAGCAATGATCATCCATCCAGCTC 2400
Oy 2544 CTGGATGACGGAATCTCTGTGTGTGGCAGCTGTAGGCAATTCAGATGAATTTGAATTT 2603
Db 2401 CTGGATGACGGAATCTCTGTGTGTGGCAGCTGTAGGCAATTCAGATGAATTTGAATTT 2460
Oy 2604 TTCCAAAGGAATGTTCTGACTGCGACAGACAGTGTCTTCCCTGATGCGCAATGCTCC 2663
Db 2461 TTCCAAAGGAATGTTCTGACTGCGACAGACAGTGTCTTCCCTGATGCGCAATGCTCC 2520
Oy 2664 ATCAGCTGATGATGAGTGTGAATTTTACTCTATAGCAATATGATTTATTTTG 2723
Db 2521 ATCAGCTGATGATGAGTGTGAATTTTACTCTATAGCAATATGATTTATTTTG 2580
Oy 2724 GTGTCTGAGACTACACACAGACTGGAGACTTTTGGTGTGATTCAGAGGAGCTGTGATG 2783
Db 2581 GTGTCTGAGACTACACACAGACTGGAGACTTTTGGTGTGATTCAGAGGAGCTGTGATG 2640
Oy 2784 AACAAATTTGCTAATGAGGCTCTTTTAAAGAAATTAACCTTTATGACTACAAAGCATG 2843
Db 2641 AACAAATTTGCTAATGAGGCTCTTTTAAAGAAATTAACCTTTATGACTACAAAGCATG 2700
Oy 2844 TGTAGAGCCAAAGAAAGCAGATGGCGCCATGCTCTGATGCTTTTAAATGCC 2903
Db 2701 TGTAGAGCCAAAGAAAGCAGATGGCGCCATGCTCTGATGCTTTTAAATGCC 2760
Oy 2904 TTCTCTGCTGCACTAAATGATGATGACAGAACTTGTCTTGTCTGCTGTGTAATTTAA 2963
Db 2761 TTCTCTGCTGCACTAAATGATGATGACAGAACTTGTCTTGTCTGCTGTGTAATTTAA 2820
Oy 2964 CTCTGCACTGAGGCACTCCGATATGACAGCTAAAGCCCAAAATTTGAAGACCTCTG 3023
Db 2821 CTCTGCACTGAGGCACTCCGATATGACAGCTAAAGCCCAAAATTTGAAGACCTCTG 2880
Oy 3024 GAGCCTTGTGATAGTAATATCCAGATTCGTTCTGTGACGCACTTCAAGGAGATTA 3083
Db 2881 GAGCCTTGTGATAGTAATATCCAGATTCGTTCTGTGACGCACTTCAAGGAGATTA 2940
Oy 3084 GGAATATTTGCTGTGAGAGCTGCTCAAGTCTTGTCTATCCAGCAATTTCCAGACAG 3143
Db 2941 GGAATATTTGCTGTGAGAGCTGCTCAAGTCTTGTCTATCCAGCAATTTCCAGACAG 3000
Oy 3144 AACCTGTTATGTTGGTGTGACAGCAGCTCTCTGTGAAATCTGTGCCCCCATCAC 3203
Db 3001 AACCTGTTATGTTGGTGTGACAGCAGCTCTCTGTGAAATCTGTGCCCCCATCAC 3060
Oy 3204 ATGCAACCATTTGAATAGATGATATGAAATCCTTAAGTGAAGCTGTAA----- 3256
Db 3061 ATGCAACCATTTGAATAGATGATATGAAATCCTTAAGTGAAGCTGTAAAGCCCCAG 3120
Oy 3257 -----GGCCAGAGATCAGAAAGGCCCCAGATCTTGTCAATGCTTCCATCT 3305
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Db 3121 AAGATCAGAGAGGCCCCAGACATCAGAAAGCCCCAGATCTTGTATGCTTCAATCT 3180
Oy 3306 GAGGAGAAATGCAAGGAGTGTGGGGTGTGCCG 3338
Db 3181 GAGGAGAAATGCAAGGAGTGTGGGGTGTGCCG 3213

RESULT 8
AAS01408
ID AAS01408 standard; cDNA; 3114 BP.
XX
AC AAS01408;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human secreted soluble alpha2delta calcium channel subunit #5 cDNA.
XX
KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
KW filter binding assay; wheat germ lectin flashplate assay; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS 1..3114
FT /tag- a
FT /partial
FT /product- "Alpha2delta calcium channel subunit #5"
FT /note- "this sequence lacks a stop codon"
XX
PN WO200119870-A2.
XX
PD 22-MAR-2001.
XX
PF 18-SEP-2000; 2000MO-EP09137.
XX
PR 16-SEP-1999; 99US-0397550.
XX
PA (WARN ) WARNER LAMBERT CO.
XX
PI Brown JP, Bertelli F;
XX
DR WPI: 2001-235262/24.
DR P-PSDB: AAU01018.
XX
PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or
PT wheat germ lectin flashplate assays -
XX
PS Claim 39; Page 70-71; 160pp; English.
XX
CC The present sequence encodes for human secreted calcium channel
CC alpha2delta subunit #5 which is soluble and retains the functional
CC characteristics of the full length or wild type alpha2delta subunit
CC (AAU01025) from which it is derived. The invention relates to truncated
CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
CC which retain their affinity for radioactively labeled gabapentin. The
CC alpha2delta subunit is 1 of the components of the heteromultimeric
CC voltage-dependent calcium channel (VDCC) complexes present in neuronal
CC and non-neuronal tissues including heart and skeletal muscle. Numerous
CC soluble forms of the human calcium channel alpha2delta subunits
CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the
CC porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are
CC described. The secreted soluble alpha2delta subunit may be used in assays
CC e.g. scintillation proximity assay (SPA), flashplate, nickel
CC filter binding or wheat germ lectin flashplate assays to detect or
CC measure the binding or interaction of a ligand (e.g. gabapentin,
CC L-leucine, L-Allo-leucine, L-methionine, L-leucine, L-isoleucine,
CC L-valine, spermine and/or L-phenylalanine) of a calcium channel
CC alpha2delta subunit.
XX
Sequence 3114 BP; 868 A; 704 C; 789 G; 752 T; 1 other:
SO

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Db 2101 TATGAGACACGCTGGCCCTCAACAATCTGAAATCTGACAAAGGCGGTGAGTGTGCC 2160
Qy 2304 TTCTCGGCACTGCCAGCGGCTCTCCAGATCAACCTGTTTGGCGGGCTGAGCAGCTC 2363
Db 2161 TTCTCGGCACTGCCAGCGGCTCTCCAGATCAACCTGTTTGGCGGGCTGAGCAGCTC 2220
Qy 2364 ACCAATGAGACTCTCTGAAAGCTGGGACACAGAAACATTTTAAACGCGACCATTTTC 2423
Db 2221 ACCAATGAGACTCTCTGAAAGCTGGGACACAGAAACATTTTAAACGCGACCATTTTC 2280
Qy 2424 CTTCTGTGATACGAGAGAGCGGCTGAGCAGATTCCAGGAGCTTCTCTACTGATCCCA 2483
Db 2281 CTTCTGTGATACGAGAGAGCGGCTGAGCAGATTCCAGGAGCTTCTCTACTGATCCCA 2340
Qy 2484 TTGAGCACTGGACCACTGATTAAGCAATGTGTGACAGCAAGTACATCCATCCAGCTC 2543
Db 2341 TTGAGCACTGGACCACTGATTAAGCAATGTGTGACAGCAAGTACATCCATCCAGCTC 2400
Qy 2544 CTGGATGACGGAATCTCTGTGTGGGACGCTGTAGCAATTCAGATGAACCTTGAATTT 2603
Db 2401 CTGGATGACGGAATCTCTGTGTGGGACGCTGTAGCAATTCAGATGAACCTTGAATTT 2460
Qy 2604 TTCCAAAGAAATTTCTGAGCTGCCAGACAGAGTGTGCTTCCCTGATGGCAATGCTCC 2663
Db 2461 TTCCAAAGAAATTTCTGAGCTGCCAGACAGAGTGTGCTTCCCTGATGGCAATGCTCC 2520
Qy 2664 ATCAGCTGTGATGATGAGACTGTGAAATTTGTACTCTCATAGACAAATATGATTTATTTG 2723
Db 2521 ATCAGCTGTGATGATGAGACTGTGAAATTTGTACTCTCATAGACAAATATGATTTATTTG 2580
Qy 2724 GTCTGTGAAGACTACACAGACTGTGAGACTTTTGGTGAGATCGAGGAGCTGTGATG 2783
Db 2581 GTCTGTGAAGACTACACAGACTGTGAGACTTTTGGTGAGATCGAGGAGCTGTGATG 2640
Qy 2784 AACAAATGCTAACAATGGGCTCTTTAAAGAAATTAACCTTTATGACTACCAAGCAT 2843
Db 2641 AACAAATGCTAACAATGGGCTCTTTAAAGAAATTAACCTTTATGACTACCAAGCAT 2700
Qy 2844 TGTAGAGCCAAACAAGAAAGACAGATGGCGCCATGGCTCTGTGATCTTATATGTC 2903
Db 2701 TGTAGAGCCAAACAAGAAAGACAGATGGCGCCATGGCTCTGTGATCTTATATGTC 2760
Qy 2904 TTCTCTCTGAGTAATAATGATCATGACAGAACTGTGTGTTCCGGGGAATTAAC 2963
Db 2761 TTCTCTCTGAGTAATAATGATCATGACAGAACTGTGTGTTCCGGGGAATTAAC 2820
Qy 2964 CTCTGCAAGTTGGTGGCACTCCGATATGACAGCTAAAGCCAGAAATTTGAACAGACCTG 3023
Db 2821 CTCTGCAAGTTGGTGGCACTCCGATATGACAGCTAAAGCCAGAAATTTGAACAGACCTG 2880
Qy 3024 GAGCCTGTGATACGTAATNTCAGCATTCGTCTCTGAGCGCACCTCAAGAGACTACA 3083
Db 2881 GAGCCTGTGATACGTAATNTCAGCATTCGTCTCTGAGCGCACCTCAAGAGACTACA 2940
Qy 3084 GGGAAATATTTGTTGTCAGACTGCTCAAGTCTTGTGTCATCCAGCAAAATTCACAACAGC 3143
Db 2941 GGGAAATATTTGTTGTCAGACTGCTCAAGTCTTGTGTCATCCAGCAAAATTCACAACAGC 3000
Qy 3144 AACCTGTTTCATGTTGGTGGTGGACAGCAGCTGCTGTGAAATCTGTGGCCGCCATCAC 3203
Db 3001 AACCTGTTTCATGTTGGTGGTGGACAGCAGCTGCTGTGAAATCTGTGGCCGCCATCAC 3060
Qy 3204 ATGGGACCATTAAGTAATGATGATATGATCCCTTAAGTGTGAACGCTTAAAG 3257
Db 3061 ATGGGACCATTAAGTAATGATGATATGATCCCTTAAGTGTGAACGCTTAAAG 3114

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RESULT 9
AAF57545
ID AAF57545 standard: DNA: 3114 BP.
XX
AC AAF57545;

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XX 11-JUN-2001 (first entry)
DT Human calcium channel alpha2delta subunit encoding DNA.
XX
DE Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
KW nervous system disorder; pain; epilepsy; anxiety; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..3114
FT /tag= a
FT
XX
PN W0200120336-A2.
PD 22-MAR-2001.
PF 18-SEP-2000; 2000MO-EP09136.
PR 16-SEP-1999; 990S-0397549.
XX (WARN ) WARNER LAMBERT CO.
XX Bertelli F, Brown JP, Dissanayake V, Suman-Chaunan N, Gee NS;
XX WPI: 2001-257902/26.
XX P-PSDB: AAB62242.
XX
PT Competitive binding assay for screening ligands which bind a cerebral
PT cortical voltage-dependent calcium channel alpha2-delta-1 subunit,
PT where the ligands identified are useful for treating disorders of the
XX nervous system, including pain .
XX
PS Disclosure: Page 70-71; 158pp; English.
XX
CC The invention relates to a new method for screening ligands which bind a
CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
CC preferably alpha2delta-1 subunit. The method comprises contacting a
CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of
CC interest and a labelled compound which binds the subunit, followed by
CC measuring the level of binding of the labelled compound to alpha2delta-1
CC subunit. The method is useful for screening ligands, preferably
CC biologically active products that modulate a nervous system function,
CC which bind a cerebral cortical voltage-dependent calcium channel
CC alpha2delta-1 subunit. The ligands identified by the method are useful
CC for treating disorders of the nervous system, including pain, epilepsy
CC and anxiety. The present sequence represents a human calcium channel
CC alpha2delta subunit encoding DNA.
XX
SQ Sequence 3114 BP; 868 A; 704 C; 789 G; 752 T; 1 other:
Query Match 82.6%; Score 3113.6; DB 22; Length 3114;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 144 ATGCCGGGCGGCGCTGCGCGCGCGGCTCCGGGGGCGCTGCGGCTTCTGCTGCC 203
Db 1 ATGCCGGGCGGCGCTGCGCGCGCGGCTCCGGGGGCGCTGCGGCTTCTGCTGCC 60
Qy 204 GGGCTTCTACGCGCGCTGGGGGACGTGTGCGCTGAGACACATACCGCTTCC 263
Db 61 GGGCTTCTACGCGCGCTGGGGGACGTGTGCGCTGAGACACATACCGCTTCC 120
Qy 264 GTGTGAAGCTCTGCGGCTTGTGGTGAGATTAATCCATTGCTGTAAGTAC 323
Db 121 GTGTGAAGCTCTGCGGCTTGTGGTGAGATTAATCCATTGCTGTAAGTAC 180
Qy 324 TCCGGTCCAGCTTCTCAAAAGAAATACAAAGATATGAGAAAGAGCTTCCCATAGAA 383
Db 181 TCCGGTCCAGCTTCTCAAAAGAAATACAAAGATATGAGAAAGAGCTTCCCATAGAA 240
Qy 384 GAAATTAATGAGCTTCAACATGTAAGAAAGCTGGCAAAAGAAACATGGAAGATGTTTAC 443

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Db 241 GAAATGATGGCTCCAAAGCTGAAGAACCTGGCAAGAACATGGAAGATGTTTCAC 300
QY 444 AAGAAGCTGAGGCGGTCAGGCGCTGTGGAGGCTGCAGAAAGACACACACCTGAACAT 503
|||||
Db 301 AAGAAGCTGAGGCGGTCAGGCGCTGTGGAGGCTGCAGAAAGACACACCTGAACAT 360
QY 504 GAATTTGATGCAGACTTACAGTATGATTAATCTTAATCTGTGCTGATTAATGAAGGAC 563
|||||
Db 361 GAATTTGATGCAGACTTACAGTATGATTAATCTTAATCTGTGCTGATTAATGAAGGAC 420
QY 564 AAGAGGGAATTTTTTTGGAGCTGGGAAAGAAATTCATCTTAAGCCCAATGACATTTT 623
|||||
Db 421 AAGAGGGAATTTTTTTGGAGCTGGGAAAGAAATTCATCTTAAGCCCAATGACATTTT 480
QY 624 AATTAATTTGCTGTGAACATCACTTAAGTACAGTCCAACTACCAACGATGTACAC 683
|||||
Db 481 AATTAATTTGCTGTGAACATCACTTAAGTACAGTCCAACTACCAACGATGTACAC 540
QY 684 AAGACCCCTGCAATTTGCAATGAGGCTTTATTTGCTGAATCTCTAAACAAAGTTTGT 743
|||||
Db 541 AAGACCCCTGCAATTTGCAATGAGGCTTTATTTGCTGAATCTCTAAACAAAGTTTGT 600
QY 744 GATACCTTGACCGTGAACCATCTCATATGACAGTACTTTGGAAGTGCAAGGCTTT 803
|||||
Db 601 GATACCTTGACCGTGAACCATCTCATATGACAGTACTTTGGAAGTGCAAGGCTTT 660
QY 804 TTTAGGCAATTCGCGGGGATTAATATGGGAACCGATGAGATGAGTCACTGCTTCGAC 863
|||||
Db 661 TTTAGGCAATTCGCGGGGATTAATATGGGAACCGATGAGATGAGTCACTGCTTCGAC 720
QY 864 TGCAGGAACCGAAATGATACATCCAGGACGAACTTCCGAAAGACCGTGCATTTTA 923
|||||
Db 721 TGCAGGAACCGAAATGATACATCCAGGACGAACTTCCGAAAGACCGTGCATTTTA 780
QY 924 GTTGACGTAGTGGCAGCATGAAAGGACTCGCTGACTATCGCGAAGCAACGCTCA 983
|||||
Db 781 GTTGACGTAGTGGCAGCATGAAAGGACTCGCTGACTATCGCGAAGCAACGCTCA 840
QY 984 TCCATTTTGGATACACTGGGGATGATGACTTCTTCAATATTTCTTATATGAGGAG 1043
|||||
Db 841 TCCATTTTGGATACACTGGGGATGATGACTTCTTCAATATTTCTTATATGAGGAG 900
QY 1044 CTTCACATATGTGAACCTTGCTGTAATGGAATTTGGTGCAGACCGACGAAACAA 1103
|||||
Db 901 CTTCACATATGTGAACCTTGCTGTAATGGAATTTGGTGCAGACCGACGAAACAA 960
QY 1104 GAGCACTTCAGGAGCATCTGACAAACTTTTCGCCAAAGAAATTTGGATATA 1163
|||||
Db 961 GAGCACTTCAGGAGCATCTGACAAACTTTTCGCCAAAGAAATTTGGATATA 1020
QY 1164 GCTCGAATGAGGCGCTTCAACATTTCTGAGTGTTCACACACAGGAGACAGAAATATC 1223
|||||
Db 1021 GCTCGAATGAGGCGCTTCAACATTTCTGAGTGTTCACACACAGGAGACAGAAATATC 1080
QY 1224 TGCAGTCAAGCCATCATCTCATACTGATGGGCGGTGGAGACACTATGATCAATCTTT 1283
|||||
Db 1081 TGCAGTCAAGCCATCATCTCATACTGATGGGCGGTGGAGACACTATGATCAATCTTT 1140
QY 1284 GCAAAATTCATTTGGCCAGATGGAAGGTTGCAATCTTCAATACCTCATTTGGAGAGAG 1343
|||||
Db 1141 GCAAAATTCATTTGGCCAGATGGAAGGTTGCAATCTTCAATACCTCATTTGGAGAGAG 1200
QY 1344 GCTGCTTTGAGACAAATCAATGAAGTGGCTGTGGCAACAAAGATTTTTTACCAG 1403
|||||
Db 1201 GCTGCTTTGAGACAAATCAATGAAGTGGCTGTGGCAACAAAGATTTTTTACCAG 1260
QY 1404 ATCTCCACTTGGCTGATGTGACAGAGAAATGTCAATGAATACCTTCAGTGTGGCGG 1463
|||||
Db 1261 ATCTCCACTTGGCTGATGTGACAGAGAAATGTCAATGAATACCTTCAGTGTGGCGG 1320
QY 1464 CCGAAAGTCATGACACAGAGCATGATGTGTGGACCGAAGCTTACATTTGACAGCACT 1523
|||||

Db 1321 CCCAAGTCATCGACGACGAGCATGATGTGTGTGAGCCAGCTTACATTTGACAGCACT 1380
QY 1524 CTGACTATGATCAGGGCCCCGTCCTGATGACACTGTAGCCATGCTGTGTTAGTAAG 1583
|||||
Db 1381 CTGACTATGATCAGGGCCCCGTCCTGATGACACTGTAGCCATGCTGTGTTAGTAAG 1440
QY 1584 CAGAAAGAAACCCAGATGGAAGGGGATCTCTGGGATGTGGTGCACAGATGTCCAGTG 1643
|||||
Db 1441 CAGAAAGAAACCCAGATGGAAGGGGATCTCTGGGATGTGGTGCACAGATGTCCAGTG 1500
QY 1644 AAGAACTTCTGAAGACCATCCCAATACAAAGTTAGGATTCAGGTTATGCTTTGCA 1703
|||||
Db 1501 AAGAACTTCTGAAGACCATCCCAATACAAAGTTAGGATTCAGGTTATGCTTTGCA 1560
QY 1704 ATCAAAATTAATGATATCTGACAGCATCCGGAATCAAGGCTGTGTACGAAGAAGA 1763
|||||
Db 1561 ATCAAAATTAATGATATCTGACAGCATCCGGAATCAAGGCTGTGTGTGTGTGTGTGT 1620
QY 1764 AAAAAAGGAAGAAACCTACTATAGTACGCTTCTCTGAGTGTGAGTGGGAAGAC 1823
|||||
Db 1621 AAAAAAGGAAGAAACCTACTATAGTACGCTTCTCTGAGTGTGAGTGGGAAGAC 1680
QY 1824 CGAGATGACGTTGAGAAATGCTATGATGATGAAAGACGGGGAAGTTTCCATGAG 1883
|||||
Db 1681 CGAGATGACGTTGAGAAATGCTATGATGATGAAAGACGGGGAAGTTTCCATGAG 1740
QY 1884 GTGAGAGACAGTGTGACAAAGGAAACGGGTTTGTGTGATGACAAATGACTATAT 1943
|||||
Db 1741 GTGAGAGACAGTGTGACAAAGGAAACGGGTTTGTGTGATGACAAATGACTATAT 1800
QY 1944 ACAGACATCAAGGCTACTCTTTCAGTTTATGTTGTGCGCTTTCAGAGTCAATGGAAA 2003
|||||
Db 1801 ACAGACATCAAGGCTACTCTTTCAGTTTATGTTGTGTGCGCTTTCAGAGTCAATGGAAA 1860
QY 2004 TATTTCTTCGAGGAGATGTAACCATGGAAGAGGCTGATGACTTAAGCAATCCCAT 2063
|||||
Db 1861 TATTTCTTCGAGGAGATGTAACCATGGAAGAGGCTGATGACTTAAGCAATCCCAT 1920
QY 2064 GTGTCTTGGCAGATGAATGCTTCTACTGACACACTGACCTACACCTGACACCGCAT 2123
|||||
Db 1921 GTGTCTTGGCAGATGAATGCTTCTACTGACACACTGACCTACACCTGACACCGCAT 1980
QY 2124 CTGTCTCACTGTAAGACGATTAAGCTCTTCACTTAAAGCAAGAAACCTTCTCTCAGTGT 2183
|||||
Db 1981 CTGTCTCACTGTAAGACGATTAAGCTCTTCACTTAAAGCAAGAAACCTTCTCTCAGTGT 2040
QY 2184 GATTAAGATTTGATCCAAAGAGCTTTTGAACGGGCTGTGAGTCCCTCCATTTGAAGG 2243
|||||
Db 2041 GATTAAGATTTGATCCAAAGAGCTTTTGAACGGGCTGTGAGTCCCTCCATTTGAAGG 2100
QY 2244 TATTTGACAGGCTGCGCTTCAACAAATCTGAAATTTGCAAGAGGCGTGGAGTGGC 2303
|||||
Db 2101 TATTTGACAGGCTGCGCTTCAACAAATCTGAAATTTGCAAGAGGCGTGGAGTGGC 2160
QY 2304 TTCTCTCGGACCTGCAACGGGCTCTTCCAGATCAACCTGTTGTGTGGGCTGAGCAGCTC 2363
|||||
Db 2161 TTCTCTCGGACCTGCAACGGGCTCTTCCAGATCAACCTGTTGTGTGGGCTGAGCAGCTC 2220
QY 2364 ACCAATCAGAGTCTCTGAAACCTGGGCAACAGGAAACATTTTAAAGCCACACATTTT 2423
|||||
Db 2221 ACCAATCAGAGTCTCTGAAACCTGGGCAACAGGAAACATTTTAAAGCCACACATTTT 2280
QY 2424 CCTCTCTGTGTACGGAAGGCGCTGAGAGATTTCCAGGAGCTTGTCTACATCAATCCCA 2483
|||||
Db 2281 CCTCTCTGTGTACGGAAGGCGCTGAGAGATTTCCAGGAGCTTGTCTACATCAATCCCA 2340
QY 2484 TTGACACATGAGACAGTCAATTAAGCAATGTGTGTGACAGCAAGTACATCCAGCTC 2543
|||||
Db 2341 TTGACACATGAGACAGTCAATTAAGCAATGTGTGTGACAGCAAGTACATCCAGCTC 2400
QY 2544 CTGATGAGAGGAATTCCTGTTGTGTGTGAGCTGTGAGGCAATTCAGATGAATCTGAATTT 2603
|||||
Db 2401 CTGATGAGAGGAATTCCTGTTGTGTGTGAGCTGTGAGGCAATTCAGATGAATCTGAATTT 2460

OY 2604 TTCCAAAGAGATTCTGAGACTGCCAGCAGACAGTGTGCTTCCCTGATGGCAATGCTCC 2663
 |||||||
 DB 2461 TTCCAAAGAGATTCTGAGACTGCCAGCAGACAGTGTGCTTCCCTGATGGCAATGCTCC 2520
 |||||||
 OY 2664 ATCAGCTGTGATGTGAGACTGTGAATTTGTTACTCATAGCAATATGATATTTATTTTG 2723
 |||||||
 DB 2521 ATCAGCTGTGATGTGAGACTGTGAATTTGTTACTCATAGCAATATGATATTTATTTTG 2580
 |||||||
 OY 2724 GTGCTGAAAGCTACACAGACTGAGACTTTTGGTGATGAGGGGCGTGATG 2783
 |||||||
 DB 2581 GTGCTGAAAGCTACACAGACTGAGACTTTTGGTGATGAGGGGCGTGATG 2640
 |||||||
 OY 2784 AACAAATTGCTAACAAATGGGCTCTTTAAAAAGAAATTACCTTTTGTGACTACCAAGCCATG 2843
 |||||||
 DB 2641 AACAAATTGCTAACAAATGGGCTCTTTAAAAAGAAATTACCTTTTGTGACTACCAAGCCATG 2700
 |||||||
 OY 2844 TGTAGAGCCCAACAGAGAAAGCAGAGATGGCGCCATGGCTCTGTGATCCTTATATGCG 2903
 |||||||
 DB 2701 TGTAGAGCCCAACAGAGAAAGCAGAGATGGCGCCATGGCTCTGTGATCCTTATATGCG 2760
 |||||||
 OY 2904 TTCCCTCTCTCAGTAATAATGATCATGACAGAACTTGTGTTCCGTGGATTTTAC 2963
 |||||||
 DB 2761 TTCCCTCTCTCAGTAATAATGATCATGACAGAACTTGTGTTCCGTGGATTTTAC 2820
 |||||||
 OY 2964 CTCTGCAAGTTGGTGGCACTCCGATATGACAGCTAAAGCCCAAGAAATTGAACAGACCCTG 3023
 |||||||
 DB 2821 CTCTGCAAGTTGGTGGCACTCCGATATGACAGCTAAAGCCCAAGAAATTGAACAGACCCTG 2880
 |||||||
 OY 3024 GAGCCTTGATATCTGATATCCAGCACTTGTCTGTAGAGCCACATCAAGAGACTACA 3083
 |||||||
 DB 2881 GAGCCTTGATATCTGATATCCAGCACTTGTCTGTAGAGCCACATCAAGAGACTACA 2940
 |||||||
 OY 3084 GGGAAATATTCCTTGTGAGAGACTGCTCCAAAGTCCCTTGTATCCAGCAAAATCCCAAGCAGC 3143
 |||||||
 DB 2941 GGGAAATATTCCTTGTGAGAGACTGCTCCAAAGTCCCTTGTATCCAGCAAAATCCCAAGCAGC 3000
 |||||||
 OY 3144 AACCTGTTATGTTGGTGTGAGACAGCAGCTGCTCTGTGAATCTGTGGCCCCCATCACC 3203
 |||||||
 DB 3001 AACCTGTTATGTTGGTGTGAGACAGCAGCTGCTCTGTGAATCTGTGGCCCCCATCACC 3060
 |||||||
 OY 3204 ATGGGACCCATTGAATATCAGGTATATGATCCCTTAAGTGTACAGCTTAAG 3257
 |||||||
 DB 3061 ATGGGACCCATTGAATATCAGGTATATGATCCCTTAAGTGTACAGCTTAAG 3114
 |||||||
 RESULT 10
 AAS01407
 ID AAS01407 standard: cDNA: 3057 BP.
 XX AAS01407:
 AC AAS01407:
 XX
 DT 04-JUL-2001 (first entry)
 XX
 DE Human secreted soluble alpha2delta calcium channel subunit #4 cDNA.
 XX
 KW Human: secreted calcium channel alpha2delta subunit: alpha2delta-2;
 KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel: VDCC;
 KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
 KW filter binding assay; wheat germ lectin flashplate assay; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key 1. Location/Qualifiers
 FT CDS 1..3057
 FT /tag= a
 FT /product= "Alpha2delta calcium channel subunit #4"
 FT /note= "This sequence lacks a stop codon"
 XX
 PN MO200119870-A2.
 XX
 PD 22-MAR-2001.

XX 18-SEP-2000: 2000MO-EP09137.
 PF
 XX
 PR 16-SEP-1999: 99US-0397550.
 XX
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Brown JP, Bertelli F;
 XX
 DR WPI: 2001-235262/24.
 DR P-PSDB: AAU01017.
 DR
 PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
 PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or
 PT Wheat Germ Lectin Flashplate assays -
 XX
 PS Claim 39: Page 69-70; 160pp: English.
 XX
 CC The present sequence encodes for human secreted calcium channel
 CC alpha2delta subunit #4 which is soluble and retains the functional
 CC characteristics of the full length or wild type alpha2delta subunit
 CC (AAU01025) from which it is derived. The invention relates to truncated
 CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
 CC which retain their affinity for radioactively labeled gabapentin. The
 CC alpha2delta subunit is 1 of the components of the heteromultimeric
 CC voltage-dependent calcium channel (VDCC) complexes present in neuronal
 CC and non-neuronal tissues including heart and skeletal muscle. Numerous
 CC soluble forms of the human calcium channel alpha2delta subunits
 CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the
 CC porcine calcium channel alpha2delta subunits (AAU01027-AAU01031) are
 CC described. The secreted soluble alpha2delta subunit may be used in assays
 CC e.g. scintillation proximity assay (SPA), flashplate, nickel flashplate,
 CC filter binding or wheat germ lectin flashplate assays to detect or
 CC measure the binding or interaction of a ligand (e.g. gabapentin,
 CC L-Norleucine, L-Allo-Isoleucine, L-methionine, L-leucine, L-Isoleucine,
 CC L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel
 CC alpha2delta subunit.
 XX
 SO Sequence 3057 BP: 848 A: 692 C: 778 G: 738 T: 1 other:
 Query Match 81.1%; Score 3056.6; DB 22; Length 3057;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3057; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 144 ATGGCGGGCGGGCTCCGCCGCCGCCGCCGCCGCCGCCGCCCTTCTCGCTGCC 203
 |||||||
 DB 1 ATGGCGGGCGGGCTCCGCCGCCGCCGCCGCCGCCGCCGCCCTTCTCGCTGCC 60
 |||||||
 OY 204 GCGCTTCTCTACGCGCGCTGGGGGAGCTGTGGCTGGAGAGCAGATACCGCTCTCC 263
 |||||||
 DB 61 GCGCTTCTCTACGCGCGCTGGGGGAGCTGTGGCTGGAGAGCAGATACCGCTCTCC 120
 |||||||
 OY 264 GTGTGTAAAGCTCTGGGCTCTGCTTTTGGTGGGAGATAAATCCATTGCTCTAAGTAC 323
 |||||||
 DB 121 GTGTGTAAAGCTCTGGGCTCTGCGCTTTTGGTGGGAGATAAATCCATTGCTCTAAGTAC 180
 |||||||
 OY 324 TCCGCTTCCACCTCTCTGCAAAAGAAATATCAAGACTATGACAAAGACGTTCCATAGAA 383
 |||||||
 DB 181 TCCGCTTCCACCTCTCTGCAAAAGAAATATCAAGACTATGACAAAGACGTTCCATAGAA 240
 |||||||
 OY 384 GAAATTTGATGGGCTCCCAACTGTTAAAGAAAGCTGGCAAGAACATGGAAGATGTTTAC 443
 |||||||
 DB 241 GAAATTTGATGGGCTCCCAACTGTTAAAGAAAGCTGGCAAGAACATGGAAGATGTTTAC 300
 |||||||
 OY 444 AAGAACTGTAGAGCCGCTCAGCGCTGTGTGAGGCTGCAAGAAAGACACACTGAAACAT 503
 |||||||
 DB 301 AAGAACTGTAGAGCCGCTCAGCGCTGTGTGAGGCTGCAAGAAAGACACACTGAAACAT 360
 |||||||
 OY 504 GAATTTGATGCAAGACTTACAGTATGATTAATCTCAATGCTGTGCTGATTAATGAAGGAGC 563
 |||||||
 DB 361 GAATTTGATGCAAGACTTACAGTATGATTAATCTCAATGCTGTGCTGATTAATGAAGGAGC 420
 |||||||
 OY 564 AAAGACGGGAATTTTGTGAGCTGGAAAGAAATTCATCTTAAGCCCAATATGACATTTT 623

|||||
Db 421 AAGAGGGGAAATTTTGGAGCTGGGAAAGAAATTCATCTTACCCCAATGACCATTTT 480
OY 624 AATAATTTGGCTGTGAACATCACTCTAAGTACGTCCCACTACCAAGCAATGTACAC 683
|||||
Db 481 AATAATTTGGCTGTGAACATCACTCTAAGTACGTCCCACTACCAAGCAATGTACAC 540
OY 684 AAGAGCCCTGCAATTTGTCAATGGGGTTTATTTGGTCAATCTCTAAACAAGTTTGTGA 743
|||||
Db 541 AAGAGCCCTGCAATTTGTCAATGGGGTTTATTTGGTCAATCTCTAAACAAGTTTGTGA 600
OY 744 GATTAATTTGACCGTGTACCCATCTCTCATATGGCAGTACTTTGGAAATGCAAGGCTTT 803
|||||
Db 601 GATTAATTTGACCGTGTACCCATCTCTCATATGGCAGTACTTTGGAAATGCAAGGCTTT 660
OY 804 TTTAGGCACTATCCGGGGATTTAAATGGGAAACAGATGAGAAAGGATGCAATGGCTTCGAC 863
|||||
Db 661 TTTAGGCACTATCCGGGGATTTAAATGGGAAACAGATGAGAAATGCAATGGCTTCGAC 720
OY 864 TGCAGAACCCGAAATGATGATACATCCAGGCAAGCAACTTCTCCGAAAGAGTGTCTATTTA 923
|||||
Db 721 TGCAGAACCCGAAATGATGATACATCCAGGCAAGCAACTTCTCCGAAAGAGTGTCTATTTA 780
OY 924 GTTGAGCTACAGTGCAGCATGAAAGAGCTCGTCTGACTATGCGGAAGCAAGTCTCA 983
|||||
Db 781 GTTGAGCTACAGTGCAGCATGAAAGAGCTCGTCTGACTATGCGGAAGCAAGTCTCA 840
OY 984 TCCATTTTGGATACACTTGGGGATGATGACTTCTCAACATATTTGCTTATATGAGGAG 1043
|||||
Db 841 TCCATTTTGGATACACTTGGGGATGATGACTTCTCAACATATTTGCTTATATGAGGAG 900
OY 1044 CTTCACATATGTGGAACCTTGCTGATGGAACCTTTGGTGCAGACCCGACAGCAACAA 1103
|||||
Db 901 CTTCACATATGTGGAACCTTGCTGATGGAACCTTTGGTGCAGACCCGACAGCAACAA 960
OY 1104 GAGCACTTCAGGAGACATCTGGACAACTTTTCCCAAGAAATGGAA TGTGGATATA 1163
|||||
Db 961 GAGCACTTCAGGAGACATCTGGACAACTTTTCCCAAGAAATGGAA TGTGGATATA 1020
OY 1164 GCTCTGAATGAGGCTTCAACATTTCTGAGTGTATTCACACCAACAGGGGACAAAGAGTATC 1223
|||||
Db 1021 GCTCTGAATGAGGCTTCAACATTTCTGAGTGTATTCACACCAACAGGGGACAAAGAGTATC 1080
OY 1224 TGCAGTCAAGCCATCATGCTCATTAACATGATGGGGGTGAGACACTATGATACATCTTT 1283
|||||
Db 1081 TGCAGTCAAGCCATCATGCTCATTAACATGATGGGGGTGAGACACTATGATACATCTTT 1140
OY 1284 GCAAAATATCAATTTGGCCAGATGGAAGTTCGATCTTCACATACCTTCATTTGGAGAGAG 1343
|||||
Db 1141 GCAAAATATCAATTTGGCCAGATGGAAGTTCGATCTTCACATACCTTCATTTGGAGAGAG 1200
OY 1344 GCTCTGTATGAGACATCTAAAGTGGATGGCCGTGGCAACAAAGATTTTATACCCAG 1403
|||||
Db 1201 GCTCTGTATGAGACATCTAAAGTGGATGGCCGTGGCAACAAAGATTTTATACCCAG 1260
OY 1404 ATCTCCACTTGGCTGATGTGACAGAGATGTCAATGAAATCTTTCACAGTCTTACCCGG 1463
|||||
Db 1261 ATCTCCACTTGGCTGATGTGACAGAGATGTCAATGAAATCTTTCACAGTCTTACCCGG 1320
OY 1464 CCCAAATCTCATCGACAGGAGCATGATGTGTGACCCGAAAGCTTTCATGACAGCACT 1523
|||||
Db 1321 CCCAAATCTCATCGACAGGAGCATGATGTGTGACCCGAAAGCTTTCATGACAGCACT 1380
OY 1524 CTGACTGATATGACGAGCCCGCTGATGACCACTGTACCATGATGCTGTGTTATGATAG 1583
|||||
Db 1381 CTGACTGATATGACGAGCCCGCTGATGACCACTGTACCATGATGCTGTGTTATGATAG 1440
OY 1584 CAGAGCAAAACAGATGGAAGGGCATCTTCTGAGAGTGGTGGCAGAGATGTGCCAGTG 1643
|||||
Db 1441 CAGAGCAAAACAGATGGAAGGGCATCTTCTGAGAGTGGTGGCAGAGATGTGCCAGTG 1500
OY 1644 AAGGAATCTTGAAGACATCCCAATACAGTTAGGATTCACGGTTATGCGCTTTGCA 1703
|||||

Db 1501 AAGAACTCTGAAGACCATCCCAATACAAAGTTAGGATTCACGGTTATGCCTTTGCA 1560
OY 1704 ATCACAATTAATGGATATATCTGACGCATCCGGAATCAGGGCTGTATGAGAAAGA 1763
|||||
Db 1561 ATCACAATTAATGGATATATCTGACGCATCCGGAATCAGGGCTGTATGAGAAAGA 1620
OY 1764 AAAAAGGGAAGAACTTAATAGTACGCTTGACCTCTCTGAGTGGAGTGGAAAGAC 1823
|||||
Db 1621 AAAAAGGGAAGAACTTAATAGTACGCTTGACCTCTCTGAGTGGAGTGGAAAGAC 1680
OY 1824 CGAGATGACGTGTTGAGAAATGCTATGTTGATGAAAGCGGGGAAAGTTTCCATGAG 1883
|||||
Db 1681 CGAGATGACGTGTTGAGAAATGCTATGTTGATGAAAGCGGGGAAAGTTTCCATGAG 1740
OY 1884 GTGAAGAGACAGTGTGACAAAGGAAACGGGTTTGGTGTATGACAAATGACTACTATTA 1943
|||||
Db 1741 GTGAAGAGACAGTGTGACAAAGGAAACGGGTTTGGTGTATGACAAATGACTACTATTA 1800
OY 1944 ACAGACATCAAGGCTACTCTTCAGTTTATAGTGTGGCGCTTTCAGAGTCAATGGGAAA 2003
|||||
Db 1801 ACAGACATCAAGGCTACTCTTCAGTTTATAGTGTGGCGCTTTCAGAGTCAATGGGAAA 1860
OY 2004 TATTTCTCGAGAGATGTAACCATCGAAGAAAGGCGCTGATGACTTTAGAACATCCCGAT 2063
|||||
Db 1861 TATTTCTCGAGAGATGTAACCATCGAAGAAAGGCGCTGATGACTTTAGAACATCCCGAT 1920
OY 2064 GTGTCTTGGAGATGAATGTCTCTACTGCAACACTGACCTACACCCCTGAGACCGCAT 2123
|||||
Db 1921 GTGTCTTGGAGATGAATGTCTCTACTGCAACACTGACCTACACCCCTGAGACCGCAT 1980
OY 2124 GTGTCTCACTTGAAGCGATTAAGCTCTACCTTAAGAGCAAGAAACCTGTCTCCAGTGT 2183
|||||
Db 1981 GTGTCTCACTTGAAGCGATTAAGCTCTACCTTAAGAGCAAGAAACCTGTCTCCAGTGT 2040
OY 2184 GATTAAGATTAATCCAAAGACCTTTTGAAGCGGGGTGATGAGCCCAATTAAGGG 2243
|||||
Db 2041 GATTAAGATTAATCCAAAGACCTTTTGAAGCGGGGTGATGAGCCCAATTAAGGG 2100
OY 2244 TATTTGACCAAGCTTGCCCTCAACAAATCTGAAATTTGACAAAGGCGCTGAGAGTGGC 2303
|||||
Db 2101 TATTTGACCAAGCTTGCCCTCAACAAATCTGAAATTTGACAAAGGCGCTGAGAGTGGC 2160
OY 2304 TTCTCTGCGACCTGCGACGCGGCTCTTCAGATCAACCTGTTTGTGCGGGCTGAGCAGCTC 2363
|||||
Db 2161 TTCTCTGCGACCTGCGACGCGGCTCTTCAGATCAACCTGTTTGTGCGGGCTGAGCAGCTC 2220
OY 2364 ACCAATCAAGACTTCTCTGAAAGCTGGGCAAGAGAACATTTTAAAGCAGACCATTTTC 2423
|||||
Db 2221 ACCAATCAAGACTTCTCTGAAAGCTGGGCAAGAGAACATTTTAAAGCAGACCATTTTC 2280
OY 2424 CCTCTCTGTTACCGAAGACCGCTGAGCAGATTCAGAGGAGCTTCTACTCGATTCCCA 2483
|||||
Db 2281 CCTCTCTGTTACCGAAGACCGCTGAGCAGATTCAGAGGAGCTTCTACTCGATTCCCA 2340
OY 2484 TTTCAGCATGTGACACAGTAAATTAAGCAATGTGTGACAGCAAGTACATCCAGCTC 2543
|||||
Db 2341 TTTCAGCATGTGACACAGTAAATTAAGCAATGTGTGACAGCAAGTACATCCAGCTC 2400
OY 2544 CTGATGTAAGCGGAATCTCTGTGGTGGCAGCTGTAGGCATTTCAAGATTAACCTGAATTT 2603
|||||
Db 2401 CTGATGTAAGCGGAATCTCTGTGGTGGCAGCTGTAGGCATTTCAAGATTAACCTGAATTT 2460
OY 2604 TTTCCAAAGGAAGTTCTGTGACTGCCAGAGACAGATGTGCTTCCCTGAGATGGCAATGCTCC 2663
|||||
Db 2461 TTTCCAAAGGAAGTTCTGTGACTGCCAGAGACAGATGTGCTTCCCTGAGATGGCAATGCTCC 2520
OY 2664 ATGAGCTGTATGATGAGACTGTGATTTGTTACTCTCATAGCAATTAATGATTTATTTTG 2723
|||||
Db 2521 ATGAGCTGTATGATGAGACTGTGATTTGTTACTCTCATAGCAATTAATGATTTATTTTG 2580
OY 2724 GTGTCTGAAGCTTACACAGACTGAGACTTTTGTGTAGATCCGAGGAGCTGTATG 2783
|||||
Db 2581 GTGTCTGAAGCTTACACAGACTGAGACTTTTGTGTAGATCCGAGGAGCTGTATG 2640

OY 984 TCCATTTGGATACACTTGGGGATGATGACTTCTTCAACATTAATTGCTTATATAGAGAG 1043
|||||
Db 841 TCCATTTGGATACACTTGGGGATGATGACTTCTTCAACATTAATTGCTTATATAGAGAG 900
OY 1044 CTTCACATATGTGAACTTCCCTGGAATGGAACCTTGTGCAAGCCGAC/GAGCAACAAA 1103
901 CTTCACATATGTGAACTTCCCTGGAATGGAACCTTGTGCAAGCCGAC/GAGCAACAAA 960
OY 1104 GACACATTCAGGAGACATCGGACAAACCTTTTGCCCAAGGAATGGAAITGGTGAATATA 1163
661 GACACATTCAGGAGACATCGGACAAACCTTTTGCCCAAGGAATGGAAITGGTGAATATA 1020
OY 1164 GCTCTGAATGAGCCCTTCAACATTTGAGTGAATTTCAACACAGCGGAC/GAAGGAATATC 1223
1021 GCTCTGAATGAGCCCTTCAACATTTGAGTGAATTTCAACACAGCGGAC/GAAGGAATATC 1080
OY 1224 TGCAGTCAGGCCATTCCTCATPACTGATGAGGCGGTGAGACATATCATACATCTTT 1283
1081 TGCAGTCAGGCCATTCCTCATPACTGATGAGGCGGTGAGACATATCATACATCTTT 1140
OY 1284 GCAAAATPACAAATGGGCAAGATCGAAGGTTTCCGATCTTCAATACCTCAATTGAGAGAG 1343
1141 GCAAAATPACAAATGGGCAAGATCGAAGGTTTCCGATCTTCAATACCTCAATTGAGAGAG 1200
OY 1344 GCTGCGTTTGCAGACATCTAAAGTGGATGGCTGTGCCAAAGGAATTTTACCAG 1403
1201 GCTGCGTTTGCAGACATCTAAAGTGGATGGCTGTGCCAAAGGAATTTTACCAG 1260
OY 1404 ATCTCCACTTGGCTGATGTGACAGAGAAATGTCANTGGAATACCTTCACCTGCTTACCCG 1463
1261 ATCTCCACTTGGCTGATGTGACAGAGAAATGTCANTGGAATACCTTCACCTGCTTACCCG 1320
OY 1464 CCCAAGTATGACACAGAGATGATGTGTGTGACACGGAAGCTTACATTGACACACT 1523
1321 CCCAAGTATGACACAGAGATGATGTGTGTGACACGGAAGCTTACATTGACACACT 1380
OY 1524 CTGACTGATGATCAGGGCCCTCCGATGACACATGATGACCATGCTGTGTTTACTAG 1583
1381 CTGACTGATGATCAGGGCCCTCCGATGACACATGATGACCATGCTGTGTTTACTAG 1440
OY 1584 CAGAAAGCAACCATGATCGAAGGGCATTTCTTGGAGTGGTGGACAGATGCTCCAGTG 1643
1441 CAGAAAGCAACCATGATCGAAGGGCATTTCTTGGAGTGGTGGACAGATGCTCCAGTG 1500
OY 1644 AAGAACTTCTGAAGACATCCCAATACAGTTAGGATTCACGGTTATGCTTTGCA 1703
1501 AAGAACTTCTGAAGACATCCCAATACAGTTAGGATTCACGGTTATGCTTTGCA 1560
OY 1704 ATCACAATTAATGRTATATCTGACGACATCCGGAACCTCAGGCTGCTGACGAAGA 1763
1561 ATCACAATTAATGRTATATCTGACGACATCCGGAACCTCAGGCTGCTGACGAAGA 1620
OY 1764 AAAAAAGCAAGAACTPACTATATAGTGTGACCTCTCTGAGGTGAGTGGGAAGAC 1823
1621 AAAAAAGCAAGAACTPACTATATAGTGTGACCTCTCTGAGGTGAGTGGGAAGAC 1680
OY 1824 CGAGATGACGTGTGAAGAAATGCTATGTGATCGAAAGACGGGAAATTTTCCATGAG 1883
1681 CGAGATGACGTGTGAAGAAATGCTATGTGATCGAAAGACGGGAAATTTTCCATGAG 1740
OY 1884 GTGAAGAAGAGTGTGAAGAAAGGAAAGGTTTGGTGTGACAAATGACACTATATAT 1943
1741 GTGAAGAAGAGTGTGAAGAAAGGAAAGGTTTGGTGTGACAAATGACACTATATAT 1800
OY 1944 ACAGACATCAAGGTAATCTTTCAGTTAGTGTGAGGCTTTTCCAGAGTCAATGGGAAA 2003
1801 ACAGACATCAAGGTAATCTTTCAGTTAGTGTGAGGCTTTTCCAGAGTCAATGGGAAA 1860
OY 2004 TATTTCTTCCAGGGAATGTAAACATGCAAGAAGGCTGCAATGACTTAGAATCCCAT 2063
1861 TATTTCTTCCAGGGAATGTAAACATGCAAGAAGGCTGCAATGACTTAGAATCCCAT 1920

OY 2064 GTGTCTTGGAGATGATGATGCTCTACTGCAACACTGACCTACACCTGAGACCCGCAT 2123
1921 GTGTCTTGGAGATGATGATGCTCTACTGCAACACTGACCTACACCTGAGACCCGCAT 1980
OY 2124 CTGTCTAGTTAGAGGATTAAGCTCTACCTTAAGAGCAAGAAAGCTCTGCTCAGTGT 2183
1981 CTGTCTAGTTAGAGGATTAAGCTCTACCTTAAGAGCAAGAAAGCTCTGCTCAGTGT 2040
OY 2184 GATAAAGAAATGATCAAGAAAGTCTTTTGGACGCGGTGTGAGTGGCCCATTTGAAGCG 2243
2041 GATAAAGAAATGATCAAGAAAGTCTTTTGGACGCGGTGTGAGTGGCCCATTTGAAGCG 2100
OY 2244 TATTGGACACGCTGGCCCTTCACAAATCTGAAAATTTCTGCAAGGCGGTGGAGTTGCC 2303
2101 TATTGGACACGCTGGCCCTTCACAAATCTGAAAATTTCTGCAAGGCGGTGGAGTTGCC 2160
OY 2304 TTCTCGGCACTGCGACGGGCTCTCCAGATCAACCTGTTTGGGGGGTGACACACTC 2363
2161 TTCTCGGCACTGCGACGGGCTCTCCAGATCAACCTGTTTGGGGGGTGACACACTC 2220
OY 2364 ACCAATCAGGACTTCTGAAAGCTGGCGACAGAGGAACAATTTTAAAGGACACATTTT 2423
2221 ACCAATCAGGACTTCTGAAAGCTGGCGACAGAGGAACAATTTTAAAGGACACATTTT 2280
OY 2424 CTTCTCTGTGTAACGAGAGCCGCTGAGCAGATTCACAGGAGCTTCTACTGATCCCA 2483
2281 CTTCTCTGTGTAACGAGAGCCGCTGAGCAGATTCACAGGAGCTTCTACTGATCCCA 2340
OY 2484 TTACGACCTGGACAGATCAATTAAGCAATGTGTTGACACAGTACATCATCCACCTC 2543
2341 TTACGACCTGGACAGATCAATTAAGCAATGTGTTGACACAGTACATCATCCACCTC 2400
OY 2544 CTGATGTAACGGAATCTCCTGTGTGGGACAGTGTGAGCAATTCAGATGAATTTGAATTT 2603
2401 CTGATGTAACGGAATCTCCTGTGTGGGACAGTGTGAGCAATTCAGATGAATTTGAATTT 2460
OY 2604 TTCCAAAGGAAGTTCTGAGCTGCCAGCAGACAGTGTGCTTCCCTGATGGAATGCTCC 2663
2461 TTCCAAAGGAAGTTCTGAGCTGCCAGCAGACAGTGTGCTTCCCTGATGGAATGCTCC 2520
OY 2664 ATACGCTGATGATGATGAGACTGTGAATTTTACCTCATAGCAATTAATGATTTATTTT 2723
2521 ATACGCTGATGATGATGAGACTGTGAATTTTACCTCATAGCAATTAATGATTTATTTT 2580
OY 2724 GTGTCTGAAGACTACACAGACTGAGACTTTTGTGTGAGATTCAGAGGAGCTGTGATG 2783
2581 GTGTCTGAAGACTACACAGACTGAGACTTTTGTGTGAGATTCAGAGGAGCTGTGATG 2640
OY 2784 AACAAATTCCTAACATGAGGCTCTTTAAAGAAATTAACCTTTATGACACCAAGCATG 2843
2641 AACAAATTCCTAACATGAGGCTCTTTAAAGAAATTAACCTTTATGACACCAAGCATG 2700
OY 2844 TGTAGAGCCCAAGAAAGAGAGAGAGAGTGGCCCATGAGGCTCTGATCTTATATGCG 2903
2701 TGTAGAGCCCAAGAAAGAGAGAGAGTGGCCCATGAGGCTCTGATCTTATATGCG 2760
OY 2904 TTCTCTCTGCAAGTAAAGATGATCAGACAGAACTGTGTTGCTGTGGGAATTTAAC 2963
2761 TTCTCTCTGCAAGTAAAGATGATCAGACAGAACTGTGTTGCTGTGGGAATTTAAC 2820
OY 2964 CTCTGCAAGTTGGTGGCACTCCGATATGACAGCTAAAGCCCAAAATTTGAAGACACCTG 3023
2821 CTCTGCAAGTTGGTGGCACTCCGATATGACAGCTAAAGCCCAAAATTTGAAGACACCTG 2880
OY 3024 GAGCCTTGTGATACGAATATCCAGATTCGTCTGAGCGCACATCAAGAGACTACA 3083
2881 GAGCCTTGTGATACGAATATCCAGATTCGTCTGAGCGCACATCAAGAGACTACA 2940
OY 3084 GGAATATTTGCTGTGAAGACTGCTCAAGTCTTGTGATCCACCAAAATCCCAAGCAGC 3143
2941 GGAATATTTGCTGTGAAGACTGCTCAAGTCTTGTGATCCACCAAAATCCCAAGCAGC 3000
OY 3144 AACCTGTTCAATGTGTGTGTGACAGACAGCTGCTCTGTGATCTGTGTGCTCCCATC 3200

Db 3001 AACCTGTCATGTCGTGTGTGAGACAGCTGCTCTGTGATCTGTGGCCCCATC 3057

RESULT 12

AAA09260 ID AAA09260 standard; cDNA: 2008 BP.

AC AAA09260:

AT 10-AUG-2000 (first entry)

DE Human alpha-2-delta-C gene 3' splice variant.

KM alpha-2-delta-C; calcium channel subunit; 3p21.1; gabapentin; cyostatic;

KW anticonvulsant; antiligrane; antiparkinsonian; antidepressant;

XX splice variant; 98.

OS Homo sapiens.

PN MO200020450-A2.

PD 13-APR-2000.

PF 07-OCT-1999: 99MO-US23519.

PR 07-OCT-1998: 98US-0103322.

PR 30-OCT-1998: 98US-0106473.

PR 29-DEC-1998: 98US-0114088.

XX (WARN) WARNER LAMBERT CO.

PI Johns MA, Moldover B, Olford JD;

DR MPI: 2000-303744/26.

XX New human nucleic acids encoding the alpha2delta-C and alpha2delta-D

PT proteins, useful in the treatment of epilepsy, migraine, chronic pain,

XX anxiety, multiple sclerosis or cancer

PS Claim 22: Page 84-85: 88pp; English.

XX The alpha-2-delta-C gene encodes a calcium channel subunit polypeptide.

CC The gene has been mapped to chromosome 3p21.1. This gene and the related

CC alpha-2-delta-D and -B genes are useful for protecting mammalian cells

CC from abnormal calcium flux by introducing expression vectors containing

CC the respective gene into mammalian cells. The antisense genes are also

CC useful for treating or preventing epilepsy. The alpha-delta-2-A protein

CC is a high-affinity binding target of the anti-convulsant drug gabapentin.

CC Therefore, alpha-delta-2 proteins may also be targeted to treat

CC seizure-related syndromes, migraine, ataxia, vestibular defects, chronic

CC pain, sleep interference, anxiety, amyotrophic lateral sclerosis (ALS),

CC multiple sclerosis, mania, tremor, parkinsonism, substance abuse or

CC addiction syndromes, mood, depression or cancer.

XX Sequence 2008 BP: 555 A; 454 C; 536 G; 462 T; 1 other:

Query Match 50.6%; Score 1908.2; DB 21: Length 2008;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1910: Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 TACTATAGGCGCGCCGCAATTCGACAGAGCGCGGAGCGAGCGAGCGAGCGCGCGC 60

DB 1 TACTATAGGCGCGCGCGCAATTCGACAGAGCGCGGAGCGAGCGAGCGAGCGCGC 60

QY 61 GCGCTGCGCCACCGCGCTCCGCGAGCTCCCGCGCGCGCTCTCTGCGCCCGCAGC 120

DB 61 GCGCTGCGCCACCGCGCTCCGCGAGCTCCCGCGCGCGCTCTCTGCGCCCGCAGC 120

QY 121 GGGGCGGTGGGAGGAGCCAGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

DB 121 GGGGCGGTGGGAGGAGCCAGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

QY 181 GGGCGTGGCGCGCTTCTGCGTCCGCGCGCTTCTCTACGCGCGCGTGGGAGCGTGGCGCT 240

DB 181 GGGCGTGGCGCGCTTCTGCGTCCGCGCGCTTCTCTACGCGCGCGTGGGAGCGTGGCGCT 240

QY 241 CGGAGCAGCAGATACCGCTCCGCGTGAAGCTCTGGGCGCGCTTCTGGGAGGAGA 300

DB 241 CGGAGCAGCAGATACCGCTCCGCGTGAAGCTCTGGGCGCGCTTCTGGGAGGAGA 300

QY 301 TAAATTCATTGCTGCTAAGTACTCCGCTCCAGCTTCTGCAAAAGAAATCAAGAGT 360

DB 301 TAAATTCATTGCTGCTAAGTACTCCGCTCCAGCTTCTGCAAAAGAAATCAAGAGT 360

QY 361 ATGAGAAAGAGTGGCCATGAAAGAAATGATGGCCCTCCAGCTGTAAGAAAGAGTGGCAA 420

DB 361 ATGAGAAAGAGTGGCCATGAAAGAAATGATGGCCCTCCAGCTGTAAGAAAGAGTGGCAA 420

QY 421 AGAATGAGAGATGTTTACAAAGAGTGGAGCGCGTGGAGCGTGGAGAGCGTG 480

DB 421 AGAATGAGAGATGTTTACAAAGAGTGGAGCGCGTGGAGCGTGGAGAGCGTG 480

QY 481 CAGAAAGACACCTGAAACATGATGAGAGCTTACAGTATGATGATCTTCAATG 540

DB 481 CAGAAAGACACCTGAAACATGATGAGAGCTTACAGTATGATGATCTTCAATG 540

QY 541 CTGTGCTGATTAATGAAAGGACAAAGCGGGAATTTTGGAGCTGGAGAAAGATTTCA 600

DB 541 CTGTGCTGATTAATGAAAGGACAAAGCGGGAATTTTGGAGCTGGAGAAAGATTTCA 600

QY 601 TCTTAGCCCAATGACCATTTTAAATTTGCTGTAACATGACTTAAGTACGCTGC 660

DB 601 TCTTAGCCCAATGACCATTTTAAATTTGCTGTAACATGACTTAAGTACGCTGC 660

QY 661 AAGTACCAAGACATGTACAAAGAGCCCTGCAATTTGCAATGGGTTTATTTGCTG 720

DB 661 AAGTACCAAGACATGTACAAAGAGCCCTGCAATTTGCAATGGGTTTATTTGCTG 720

QY 721 AATCTTAACCAAGTTTGTGATTAATTTGAGCTGAGCCGATCTCTCATATGAGAGT 780

DB 721 AATCTTAACCAAGTTTGTGATTAATTTGAGCTGAGCCGATCTCTCATATGAGAGT 780

QY 781 ACTTTGAGAGTGCAGAGGCTTTTATGAGCATATCCGGGATTTAAATGGAACACATG 840

DB 781 ACTTTGAGAGTGCAGAGGCTTTTATGAGCATATCCGGGATTTAAATGGAACACATG 840

QY 841 AGATGAGTCAATTCCTTCTGACTGACGAGAACGAAATGTAATCCAGCAGCACTT 900

DB 841 AGATGAGTCAATTCCTTCTGACTGACGAGAACGAAATGTAATCCAGCAGCACTT 900

QY 901 CTCCGAAAGCGTGGTCAATTTAGTGAAGCTCAAGTGGGAGATGATGACTTCTTCA 960

DB 901 CTCCGAAAGCGTGGTCAATTTAGTGAAGCTCAAGTGGGAGATGATGACTTCTTCA 960

QY 961 CTATCCGAGAGCAAGAGTCTCATCTTCTGATCACTTGGGAGATGATGACTTCTTCA 1020

DB 961 CTATCCGAGAGCAAGAGTCTCATCTTCTGATCACTTGGGAGATGATGACTTCTTCA 1020

QY 1021 ACATTAATGCTTAATATGAGAGCTTCACTATGAGAGCTTCTGAAATGGAATCTTGG 1080

DB 1021 ACATTAATGCTTAATATGAGAGCTTCACTATGAGAGCTTCTGAAATGGAATCTTGG 1080

QY 1081 TGCAGCGCAGAGCAAGCAAAAGAGAGCTTCAAGGAGATCTGAGCAAACTTTTGGCA 1140

DB 1081 TGCAGCGCAGAGCAAGCAAAAGAGAGCTTCAAGGAGATCTGAGCAAACTTTTGGCA 1140

QY 1141 AAGGATTTGGAATGTTGATATAGCTCTGAATGAGAGCTTCAACATTTGAGGATTTCA 1200

DB 1141 AAGGATTTGGAATGTTGATATAGCTCTGAATGAGAGCTTCAACATTTGAGGATTTCA 1200

QY 1201 ACCACAGGAGACAGAGATATCTGAGTCAAGCCATCATGCTCATMACTGATGGGCGG 1260

DB 1201 ACCACAGGAGACAGAGATATCTGAGTCAAGCCATCATGCTCATMACTGATGGGCGG 1260

QY 1261 TGGACACCTATGATCAATCTTTGCAAAATACAAATTTGGCAGATGCAAGGTTCCGATCT 1320

Db 308 AAATGAAGGACAAAGACGGAAATTTTGGAGCTGGGAAGAAATTCATTAGCCCC 367
 QY 611 AAATGACCATTTAAATATTTGGCTGTGAACATCAGTCTAAGTACGTCCAAAGTACCAC 670
 Db 368 AAATGACCATTTAAATATTTGGCTGTGAACATCAGTCTAAGTACGTCCAAAGTACCAC 427
 QY 671 GAACATGTACAAAGAACCCCTGCAATGTCAATGGGTTTATGTGCTCAATCTCTAAA 730
 Db 428 GAACATGTACAAAGAACCCCTGCAATGTCAATGGGTTTATGTGCTCAATCTCTAAA 487
 QY 731 CAAGTTTTTGTAGATTAACCTTTCAGCCGTCATCTCATATATGAGTACTTTGGAAG 790
 Db 488 CAAGTTTTTGTAGATTAACCTTTCAGCCGTCATCTCATATATGAGTACTTTGGAAG 547
 QY 791 TGGAAAGGGCTTTTATAGGAGTATCCGGGGATTTAAATGGGAACCAATAGATGAGT 850
 Db 548 TGGAAAGGGCTTTTATAGGAGTATCCGGGGATTTAAATGGGAACCAATAGATGAGT 607
 QY 851 CATTTGCCCTTCGACTGAGAGAACCGAAATGTGTACATCCAGGACCACTTCTCGAAGA 910
 Db 608 CATTTGCCCTTCGACTGAGAGAACCGAAATGTGTACATCCAGGACCACTTCTCGAAGA 667
 QY 911 CGTGTCAATTTTATGTTGACGCTCAGTGGCAGCATGAAGAAGACTCCGCTGACTATCGGAA 970
 Db 668 CGTGTCAATTTTATGTTGACGCTCAGTGGCAGCATGAAGAAGACTCCGCTGACTATCGGAA 727
 QY 971 GCAAGAGTCTCATTCATTTTGGATACACTTGGGGATGATGACTCTTCAACATTAATGC 1030
 Db 728 GCAAGAGTCTCATTCATTTTGGATACACTTGGGGATGATGACTCTTCAACATTAATGC 787
 QY 1031 TTATTAATGAGAGACTTCACATNTGTGMAACCTTGCCTGAATGAACCTTTGGTGAAGCGGA 1090
 Db 788 TTATTAATGAGAGACTTCACATNTGTGMAACCTTGCCTGAATGAACCTTTGGTGAAGCGGA 847
 QY 1091 CAGGACAAACAAAGAGACACTTCAGGGAGCATCTGGACAAACTTTTGGCCAAAGGAATGG 1150
 Db 848 CAGGACAAACAAAGAGACACTTCAGGGAGCATCTGGACAAACTTTTGGCCAAAGGAATGG 907
 QY 1151 AATGTTGATATAGTCTCTGTAATGAGGCGCTTCAACATTTCTGAGTATTCACACACGCGG 1210
 Db 908 AATGTTGATATAGTCTCTGTAATGAGGCGCTTCAACATTTCTGAGTATTCACACACGCGG 967
 QY 1211 ACAAGGAAATATCTGCAAGTCCAGGCAATCATGCTCATTAACCTGATGGGCGGTGACACCTTA 1270
 Db 968 ACAAGGAAATATCTGCAAGTCCAGGCAATCATGCTCATTAACCTGATGGGCGGTGACACCTTA 1027
 QY 1271 TGTATCAATCTTTGCAAAATACATATTGGCCAGATCGAAGGTTTGCATCAATACCT 1330
 Db 1028 TGTATCAATCTTTGCAAAATACATATTGGCCAGATCGAAGGTTTGCATCAATACCT 1087
 QY 1331 CATTTGACGAGAGGCTGCGCTTTCAGACAAATCTAAAGTGGATGGCGTGGCCAAACGAAG 1390
 Db 1088 CATTTGACGAGAGGCTGCGCTTTCAGACAAATCTAAAGTGGATGGCGTGGCCAAACGAAG 1147
 QY 1391 ATTTTATACCGAATCTCCACCTTGGCTGATGTGACAGGAATGTCAATGAAATACCTTCA 1450
 Db 1148 ATTTTATACCGAATCTCCACCTTGGCTGATGTGACAGGAATGTCAATGAAATACCTTCA 1207
 QY 1451 CGTGCTTACCGGCGCCAAAGTATCATGACAGAGCATGTATGTGTCGACCGAAGCTTAA 1510
 Db 1208 CGTGCTTACCGGCGCCAAAGTATCATGACAGAGCATGTATGTGTCGACCGAAGCTTAA 1267
 QY 1511 CATTTGACGAGCT-----CTGACTGATGATCAGGCGCGCTCTCTGAT 1552
 Db 1268 CATTTGACGAGCTCTTCCCTCAGGACAAAGCTGACTGATGATCAGGCGCGCTCTCTGAT 1327
 QY 1553 GACCACTGTAGCCATGCTCTGTGTTAGTAAGCAGAGCAAGAACCATGATCAAGGGCATTTCT 1612
 Db 1328 GACCACTGTAGCCATGCTCTGTGTTAGTAAGCAGAGCAAGAACCATGATCAAGGGCATTTCT 1387
 QY 1613 TCTGGAGAGTGTGGCAGACAGATGTCCCACTGAAAGAACTTCTGAAAGCACCATCCCAATA 1672
 Db 1388 TCTGGAGAGTGTGGCAGACAGATGTCCCACTGAAAGAACTTCTGAAAGCACCATCCCAATA 1447

QY 1673 CAAAGTTAGGAGATTCAGGCTTATGCTTTCGAATCACAATAATATGRTATATCCGACGCA 1732
 Db 1448 CAAAGTTAGGAGATTCAGGCTTATGCTTTCGAATCACAATAATATGRTATATCCGACGCA 1507
 QY 1733 TCCGGAAGTACAGGCTGCTGTACGAAGAAGAAAAAGCGAAGAAACCTAATATAGTAG 1792
 Db 1508 TCCGGAAGTACAGGCTGCTGTGTACGAAGAAGAAAAAGCGAAGAAACCTAATATAGTAG 1567
 QY 1793 CGTTGACCTCTCTGAGGTGGAAGTGGGAAGACCGAGATGACGTGTGGAATGCTATGTT 1852
 Db 1568 CGTTGACCTCTCTGAGGTGGAAGTGGGAAGACCGAGATGACGTGTGGAATGCTATGTT 1627
 QY 1853 GAATCGAAGACGGGGAAGTTTCCATGAGAGGTGAAGAAGACAGTGGACAAAGGGAAG 1912
 Db 1628 GAATCGAAGACGGGGAAGTTTCCATGAGGTGAAGAAGACAGTGGACAAAGGGGTACA 1687
 QY 1913 GGTCT 1917
 Db 1688 TTTT 1692
 RESULT 14
 AAS17582
 ID AAS17582 standard; cDNA; 3445 BP.
 XX
 AC AAS17582:
 XX
 DT 26-FEB-2002 (first entry)
 XX
 DE DNA encoding novel secreted protein #11.
 XX
 KW Secreted protein; cytosolic; immunosuppressive; vulnary; vaccine;
 KW antiinflammatory; neuroprotective; nephrotoxic; cardiovascular;
 KW human; cancer; autoimmune disease; wound healing disorder; infection;
 KW hematopoietic disorder; inflammatory disorder; infertility;
 KW neurological disease; psychiatric disease; cardiovascular disease;
 KW respiratory disease; renal; gastrointestinal; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..3445
 FT /tag= a
 FT /product= "human secreted protein"
 XX
 PN WO200179454-A1.
 XX
 PD 25-OCT-2001.
 XX
 PF 11-APR-2001: 2001WO-US11797.
 XX
 PR 13-APR-2000: 2000US-196603P.
 PR 24-APR-2000: 2000US-199417P.
 XX
 PA (SMK) SMITHKLINE BEECHAM CORP.
 PA (SMK) SMITHKLINE BEECHAM PLC.
 XX
 PI Agarwal P, Murdoch PR, Ritzvi SK, Smith RF, Xiang Z;
 PI WPI: 2002-061975/08.
 DR P-PSDB: AAU09870.
 XX
 PT New secreted proteins or polypeptides, useful for treating e.g. cancer,
 PT autoimmune diseases, wound healing disorder, infections, haematopoietic
 PT disorders, inflammatory disorders, infertility, cancer
 XX
 PS Claim 2: page 42-44; 92pp; English.
 XX
 CC The invention relates to an isolated novel secreted polypeptide (I) and
 CC polynucleotide (II). (I) and (II) are useful for treating cancer,
 CC autoimmune diseases, wound healing disorder, infections, haematopoietic
 CC disorders, inflammatory disorders, infertility, neurological and

CC psychiatric diseases, cardiovascular diseases, respiratory diseases, renal diseases, or gastrointestinal diseases. These may also be used to treat diseases, abnormalities and disorders caused by abnormal expression, production, function and/or metabolism of the genes, as vaccines for inducing immunological response in a mammal, and in screening methods for detecting the effect of added compounds on the production of mRNA and polypeptide in cells. The polypeptides can be used as immunogens to produce antibodies immunospecific for the polypeptides, and to identify membrane-bound or soluble receptors. The polynucleotides may be used as diagnostic reagents, in chromosome localisation studies, CC and in tissue expression studies. The present sequence represents the CC coding sequence of novel human secreted protein #11.

XX Sequence 3345 BP; 772 A; 943 C; 960 G; 670 T; 0 other;

Query Match 33.6%; Score 1268.2; DB 24; Length 3345; Best local Similarity 63.8%; Pred. No. 1.3e-277; Matches 2010; Conservative 0; Mismatches 1118; Indels 21; Gaps 5;

250 AGATACCGCTCTCCGTGGTGAAGCTCTGGGCTTCGGCTTTGGTGGGAGATAAATCCA 309
 161 AGATTCTCTGGAACAGTGAAGCTATGGGCTGACACCTTCGGGGGACCTGTATACCA 220
 310 TTGCTCTAGTACTCCGCTTCCAGCTTTGCAAAAGAAATACAAAGATAGAGAAAG 369
 221 CTGTGACCAAAATAGTACGGCTCTCTCTGCTGAGAAAGATACAAAGATGTGAGTCCA 280
 370 ACCTTCCATAGAAATATGATGGCTCCAGCTGCTGAAGAAAGTGGCAAAACATGG 429
 281 GTCTGAAGATCGAGAGGTGATGGCTGAGGTGAGAGAAATCTTGAAGACATGG 340
 430 AAGAGATGTTTCAAGAAAGTCTGAGGCCCTGAGGCTGTGTGAGAGCTGCAAGAAAG 489
 341 AGAACATGCTGCGGAGGAAGTGGAGCGGTCCAGATCTGGTGAAGATCTGCCGAGAGG 400
 490 CACACCTGAAACATGATTTGATGCAAGCTTACAGTATGATATCTTCAATGCTGTGCTGA 549
 401 CCACCTGGAACCGAATTCATGAATCCCTGTGCTGCAATATCA/CTCGCTCTGA 460
 550 TAAATGAAGGCAAGAGGGAATTTTGGAGCTGGGAAGGAATTCATCTTACGCC 609
 461 TCACAGAGAGGAGGAGGAGCACTTGTGAGCTGGGCGCCGAGTTCCTCTGGAGT 520
 610 CAAATGACATTTTAAATATTTGCTGTAACATCAGTCTAAGTGAAGTCAAGTACCA 669
 521 CCAATGCTCACTTCAACACCTGCGGTGAACCTCCATCAGCAGACCTGACACTGCCA 580
 670 CCAATGCTCAACACACCTGCAATGCTCAATGGGCTTATTTGCTTGAATCTCTAA 729
 581 CCAAGCTGTAACAAAGACCGAGATATTTTAAATGAGCTCAATGCTTGAAGCTTGA 640
 730 ACAAGTTTTTATAGATATCTTGACCCGACCAATCTCTCATNAGGCACTATTGGAA 789
 641 ATGCTGCTCTCTGAGAACTTCCAGAGAGACCAACGTTGACCTGGCAATTTTGGGA 700
 790 GTCAAAAGGCTTTTATGAGCAGTATCCGGGATTAATATGGAACAGATGGAATGAG 849
 701 GTGCAACTGATTTTCAAGGATCTATCCAGATATAAATGAGACCTGATGGAATGAG 760
 850 TCATGCTCTGACCTGAGGAACCAAAATGATATCCAGCAGCAACTTTCGGAAG 909
 761 TCATTACTTTGACGCGGAAACCGGGCTGTATCAATCAACCTCTACTTCTCCCAAG 820
 910 AGCTGATTTTATGATAGCTAGTGGCAGATGAAGAGATCCGCTGACTATACGCA 969
 821 ACATAGTATTTTGTGACGAGTGAAGGAGATGAAGGGCTGAGAGACTTATTTGCA 880
 970 AGCAAAAGCTCATCTATTTGATACATCTGGGATGATGACTTCTCAACATATG 1029
 881 AGCAGACCATCACACCTTTGACACCTGGGGAGATGACTTCTAATATATCATAG 940
 1030 CTATTAATGAGAGGCTTCAATATGTGAACTTGCCTGAATGAAGCTTGTGCAAGCCG 1089

941 CGTAAATGACTACGCTTCATTCAGAGCTGTGTTTAAAGGATCTCGTCCAGGGG 1000
 1090 ACAGACAAACAAAGAGACTTTCAGGAGCATCTGAGCAAACTTTGGCCAAAGAAATG 1149
 1001 ACCGAGCAATCGAGAGATTTTCAAACTGCTGGGAGAGATTTATGATCAAAAGGTGG 1060
 1150 GAATGATGATATGCTCTGAATGAGGCTTCAACATTTCTAGTATGATTTCAACACAGG 1209
 1061 GGGTCTGAGCAAGCCCTGAGAGAGCTTCCAGATCTGAGACATGTTCCAAAGGCCA 1120
 1210 GACAGAAAGTATCTGAGTCAAGGCAATCATCTCATTAATGATGGGCGGTGACACT 1269
 1121 AGCAAGAAAGCTCTGCAACAGGCATCATCTCATCAGAGAGGCGGTGAGAGCT 1180
 1270 ATGATACATCTTTGCAAAATACATTTGGCCAGATTCGAAGGTTGCAATCTTCAATACC 1329
 1181 ACAGCGGCTTTGAGAAAGATTAACGTGGCCAGCATGATGATGCTCGAGTTTCACTTACC 1240
 1330 TCATTGACAGAGGCTGCGCTTTCAGACAAATCTAAAGTGGATGGCTGCAACAAAG 1389
 1241 TCATTGGAGAGAAAGTGTCTTTTCTGACCGCATGAAAGTGTGATTCATCAACAAAG 1300
 1390 GATTTTACCAGATCTCCACCTTGGCTGATGTCAGAGAAATGTCATGGAATACCTTC 1449
 1301 GCTACTACAGCAGATCTCAACGCTGGCGGACACCGAGGAAGATGATGGAATACCTGC 1360
 1450 ACCTGCTTACCGGCGCCCAAAAGTATGACCAAGAGCATGATGTGTGACCGAAGCTT 1509
 1361 ACCTGCTACAGCGCGCCCGCTGATCAACAGCACAGCATCATGCTGAGACAGAGCTT 1420
 1510 ACATTTGACAGCTCT-----GACTGATGATGAGGCGCCGCTGATGACCACTGTAG 1563
 1421 ACATGACAGCAAGCTCTCTAAGCTCGAGGCTGAGACCTGACATCTCAACCTGTGG 1480
 1564 CCATGCTGTGTTTATGATGACAGAGCAAGCAAGATGAGAGGCTTCTGTGGAGTGG 1623
 1481 CCATGCGAGCTTCAAGCAAGAGCAAGAAAGCATGATGATGATCTCTGTGGTGG 1540
 1624 TTGGCAGAGATGCCAGTGAAGAAAGTCTGAAAGCAATCCCAATACAGTTAGGA 1683
 1541 TGGGCTGATGATGAGGCTTGAAGAGCTGATGAAGCTGGGCGCCGCTACAGCTTGGAG 1600
 1684 TTTCAGGTTATGCTTTGCAATCAAAATATGATGATCTGAGCAGTCCGGAATCA 1743
 1601 TGCAGGATAGGCTTTCTTAACACCAAAATGCTATCATCTCTCCATCCGAGCTCC 1660
 1744 GAGTCTGTACGAAGAAAGAAAAAGGAA---GAAACCTTAATATGATGAGCTTGACC 1800
 1661 GGCCTGCTACAGAGAGGGAAGAAACTAAACCTTAATACCAAGTGTGATC 1720
 1801 TCTCTAGGTGAGTGGGAGACCGAGATGACGTGTTGAGAAATGCTATGATGAAATCGAA 1860
 1721 TCTCCAGAGTGGAGTGGGAAGACAGGCTGAATCTTGAGAACAGCATGATCAATAGGG 1780
 1861 AGACGGGGAAGTTTCCATGAGAGGTGAAGAGACATGAGCAAGAGGAAAGGGTTTGG 1920
 1781 AAACAGGATCTCTCTGATGAGATGTAAGGTTCCGATGATAAAGGGAAGCGATCTTT 1840
 1921 TGATGCAATGACTACTTATATACAGATCAAGGATCTCTTCACTTATAGTGTGG 1980
 1841 TCTGACCAATGACTACTTCTTACAGGATCATGAGCAGACCCCTTTCACTTTGGGGTGG 1900
 1981 CGCTTTCAGAGGTCAAGGAAATATTTCTTCCGAGGAATGTAAACATGGAAGAGCC 2040
 1901 TCTGTCCCGGGGCAAGGAGATACATCTTCTGGGAAACAGCTGTGGAAGAGGCC 1960
 2041 TGCATGACTTAAACATCCCGATGCTCTTGGCAGATGAATGCTCTCTCAACACTG 2100
 1961 TGCATGACTTGTCTTACAGACCTGCGCTTGGCGCTGACAGATCTTACTCATCAG 2020
 2101 ACCTACACCTGAGCAGCGCATCTGTCTCACTTGAAGCGATTAAGCTCTACCTAAAG 2160
 2021 ATATTGACCCAGACAGCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCTCAGCA 2080

OY	2161	GC	AAAGAACTCTGCTCCAGTGTGATTAAGATTGATTC	AAAGAAAGTCCCTTTTGA	CGCG	2220
Db	2081	GGA	AGGACCCAGACCTGGAGTGTACAGAGAGCTGTGTCGGAGGTGCTGTTT	ACGGG	2140	
OY	2221	TGG	GACTGGCCCCATTGAAAGCGTATTTGGACACACCTGCCCCCTCAACAAT	CTGMAAAT	2280	
Db	2141	TGG	GACAGCCCCCATGGAAAGCTTACTGGACAGCGCTGGCCCTCAACATG	TCACAGAGT	2200	
OY	2281	CTG	CAAGGGCGTGGAGGTGGCTTCTCCGCGACTGCGACGGGCGTCCGGAAT	CAAC	2340	
Db	2201	CTG	AAACGTTGGTGGACATGGCTTCTGGGCACCCGGGCTGCGCTCTG	MAAGCACT	2260	
OY	2341	TG	TTTTCGGGGGCTGAGCACTCAACAATGACACTTCTG	MAAGCTGGCCACAAGAGA	2400	
Db	2261	TG	TTTCGGGGCTCCGAGAAAGTCTCCAGACGAAGTTCCTGACAC	CTGAGACGAGGCCA	2320	
OY	2401	AC	ATTTTAAACGAGACACATTTCCCTCTCTGTTACCGAAGCGGCTGAGCA	ATTCCAG	2460	
Db	2321	GCG	GTTCACCCCTGGAGACCGGCTTCCCGTGGTGAACCGCAGGGCTC	GAGATCTCTCG	2380	
OY	2461	GGA	CTTTCGTCTACTCGATCCCATTCAGCACTGGAGCA	GTCA-----ATTAAGCAATG	2514	
Db	2381	GCA	GCTTCGCTTCAACCTCGCGTGGGCACAAAGACACCAAGAAAGTGGG	TGAACCCATGG	2440	
OY	2515	TGG	TACAGCAAGTACATTCATCCAGCTCCTGATGAAGGAAATCTCTG	TGGTGACAG	2574	
Db	2441	TGG	TACGCGACMACAGCTGTGGCGGTGACCGTGGACAGAGAGACAGC	ATTGCTGTCAG	2500	
OY	2575	CTG	TAGGCATTGAGTGAACCTGGAATTTTCCAAAGGAAGTTCTGGAC	TGCCACGACAG	2634	
Db	2501	CGC	GGGCGCTCCAAATGAACTGGAAATTCCTCCAGCGCAATTTCTGG	CGGCAACGGCG	2560	
OY	2635	AGT	GTGCTTCCCTGGATGGCAATGCTCCATACAGCTGTGATGAGAC	CTGTGAATGTT	2694	
Db	2561	AGT	GACGACACTGTGGATGGGCCGCTGCACACAGACTGCCAGAGAC	AGTATCTGGACTGCT	2620	
OY	2695	ACCT	CACTAGACAATAATGATTTATTTTGGTGTCTGAAGACTACACAG	ACTGTGACACT	2754	
Db	2621	TGCT	GTATCACAACAACAGGGGTTCTATTTGATCTTCCAAGAGTCCG	AGACGGGAAGAT	2680	
OY	2755	TTTT	TGGTGAAGTCCGAGGAGCTGTGATGAACAATTTGCTAACAA	TGGGCTCCTTTAA	2814	
Db	2681	TTCT	GGGAGGGTGGATGTGTGCTCTTAACCCAGCTGTCACACATGG	GGGTGTTACGC	2740	
OY	2815	GAA	TTACCTTTATGATCTACCAAGCCATGTGTGAGCACAACAGAA	GAGAGGATGGCG	2874	
Db	2741	AA	GTGACTATGATATGACTATACAGGCATGTGCAACCCCTGCA	GTCAACACACATGTGAC	2800	
OY	2875	CCCA	TGGGCTCTCGATCTTTAATGCTTCTCTCTGACAGTAAATGG	ATCATGACAG	2934	
Db	2801	CCC	AGCCCCCTGGTCAAGCCCCCAATTTTGGCTTCTTGAACGGG	AGCAGAGTGGCGCG	2860	
OY	2935	AACT	GTGCTGTTTCCGTTGGTGAATTTAACTCTGCAAGTTGGTGG	CACTCCGATATACAG	2994	
Db	2861	AGCT	GCTGCTGTCTCGCTGAGGTGAAGTGTCTGGGGCTCTGTG	TACGACAGAGGGCGCG	2920	
OY	2995	CTA	AAAGCCCAAAATTTGAAGACAGA---CCCTGGAGCCCTGTG	TACTGTAATACAGCAT	3051	
Db	2921	AGG	CCACAAACAACAAGAAAGACAGACCCGCTGCAAGCTTCG	CACAGAGTACCCCTGT	2980	
OY	3052	TGCT	TTCTGAGGCACTCAAGAGACTACAGGGAATTTGCTTTG	TGAAGACTGCTCCA	3111	
Db	2981	TGCT	TACACAGCGGCACTCCGGAGGCAACGGGATGCTGG	AGTGGCGGCTGCA	3040	
OY	3112	AGT	CTTTGTATCCAGCAATCCCAAGACGCAACCTGTTCA	TGTGTGGTGACAGA	3171	
Db	3041	AGG	TATTTGTGTGAGAGATTTCCCAACAGTAACTCTCT	CTCGTGTGACAGACCCA	3100	
OY	3172	GCT	GCTCTG---TGAATCTGTGGGCCCATACCATGGCAC	CAATGAATCAGATATA	3228	
Db	3101	CTT	CTCGAAGATGGGCTTCGGCTCTGAGATATTAACCTT	AACTGAGTGTCTGACATA	3160	

OY 3229 ATGATCCCTTAATGTGGAAAGCTTAAAGGCCAGAAATACGAAGGGGCCAAGACTTT 3288
 ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
 Db 3161 ATGCCTCTGTCAATGTGGAACCGGATCGCTCCCGAAGCTCCGCGGGGACACAGACTCT 3220
 ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
 OY 3289 GTCATGCTTCATCCTCGAGAGAATGCAAGGAGTGTTGGGGTTCGGCGAGTCTCCAG 3348
 ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
 Db 3221 GCCACGCTTTCATCCAGAGAAATAATGCCAGGACTCGGGCGGCGCTTGGAACAACCTCAG 3280
 ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
 OY 3349 CCCAGACAGTCTCTCTCTCTCTCTCTG 3377
 ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
 Db 3281 CTTGCGCGCCCTACTCTCTCTCTCTG 3309

RESULT 15
AAA09254
ID AAA09254 standard; cDNA; 5073 BP

AC	AAA09254;
XX	
DT	10-AUG-2000 (first entry)
XX	
DE	Human alpha-2-delta-D gene.
XX	
KW	alpha-2-delta-D; calcium channel; 12p13.3; gabapentin; cytoskeletal; K+
KW	anticonvulsant; antimigraine; antiparkinsonian; antidepressant; ss
XX	
SS	Homo sapiens.

PH	Key	Location/Qualifiers
FT	CDS	3..3365
FT		/*tag= a
XX		
PN		WO200020450-A2.

XX		
PD	13-APR-2000.	
XX		
PF	07-OCT-1999;	99WO-US23519
XX		
PR	07-OCT-1998;	98US-0103322
PR	30-OCT-1998;	98US-0106473
PR	29-DEC-1998;	98US-0114088

PI	Johns MA,	Moldover B,	Offord JD;
XX			
DR	WPI; 2000-303744/26.		
DR	P-PSDB; AAY92321.		

PT New human nucleic acids encoding the alpha2delta-C and alpha2delta-D proteins, useful in the treatment of epilepsy, migraine, chronic pain, anxiety, multiple sclerosis or cancer

PS Claim 1; Page 64-66; 88pp; English.

CC The alpha-2-delta-2 gene encodes a calcium channel subunit polypeptide.
CC The gene has been mapped to chromosome 12p13.1. This gene and the related
CC alpha-2-delta-C and -B genes are useful for protecting mammalian cells
CC from abnormal calcium flux by introducing expression vectors containing
CC the respective gene into mammalian cells. The antisense genes are also
CC useful for treating or preventing epilepsy. The alpha-delta-2-A protein
CC is a high-affinity binding target of the anti-convulsant drug gabapentin.
CC Therefore, alpha-delta-2 proteins may also be targeted to treat
CC seizure-related syndromes: migraine, ataxia, vestibular defects, chronic
CC pain, sleep interference, anxiety, amyotrophic lateral sclerosis (ALS),
CC multiple sclerosis, mania, tremor, parkinsonism, substance abuse or
CC addiction syndromes, mood, depression or cancer.

Sequence	5073	BP:	1280	A;	1390	C;	1347	G;	1056	T;	0	other;
Query Match	33.68;	Score	1268.2;	DB	21;	Length	5073;					
Best Local Similarity	63.68;	Pred. No.	1.5e-277;									
Matches 2015: Conservative	0;	Mismatches	113;	Indels	39;	Gaps	4					

QY	250	AGATACCGCTCTCCGTTGTAAGCTCTGGGCGCTGGCTTTTGTGGGGAGATATAATATCA	309
Db	163	AGATTCCTTGAAACAGATGAAGCTATGGGCTGACACCTTGGGGGGACCTGTATATACA	222
QY	310	TTTGCTGTAAGTACATCCGTTTCCACGCTTTCGCAAAAGAAATACAAAGAATAGAGAAG	369
Db	223	CTGTGACCAAAATACATCAGGCTCTCTCTTTCGTCAGAAAGAAATACAAAGATGTGAGTCCA	282
QY	370	ACGTTCCCTATGAAGAAATTTGATGGCCCTCCAACTGGATTAACAACTGGCAAAAGACATGG	429
Db	283	GTCTGAAGTTCAGAGAGCTGGATGGCTTGGAGCTGGTGGAGAAATTTCTCAGAGACATGG	342
QY	430	AAGAGATGTTTTCACAAGAAGTCTGAGGCCCTCAGGCGCTGTGGTGGAGGCTGCAGAAAG	489
Db	343	AGAAATCTGTGGGAGGAAAGTTCAGAGGGCGTCCAGAAATCTGTGTGAAGATTCGCCAGAGG	402
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GenCore version 5.1.5
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Total number of hits satisfying chosen parameters: 1419640

Minimum DB seq length: 0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	3604.8	95.6	3690	US-10-162-012-14	Sequence 14, Appl
2	3604.8	95.6	3690	US-09-875-423-1	Sequence 1, Appl
3	3378.2	89.6	3528	US-09-728-628-12	Sequence 12, Appl
4	3229.6	85.7	3276	US-10-162-012-16	Sequence 16, Appl
5	3229.6	85.7	3276	US-09-875-423-3	Sequence 3, Appl
6	419	11.1	519	US-09-563-817-794	Sequence 794, Appl
7	387.2	10.3	667	US-09-924-340-99	Sequence 99, Appl
8	387.2	10.3	667	US-09-992-600A-99	Sequence 99, Appl
9	214	5.7	5463	US-10-116-949-1	Sequence 1, Appl
10	214	5.7	5463	US-10-116-949-3	Sequence 3, Appl
11	206.4	5.5	5279	US-10-116-949-5	Sequence 5, Appl
12	135.4	3.6	1217	US-10-050-786-4	Sequence 4, Appl
13	130.6	3.5	3055	US-10-090-827-11	Sequence 10, Appl
14	130.6	3.5	3109	US-10-090-827-11	Sequence 11, Appl
15	130.6	3.5	3190	US-10-090-827-12	Sequence 12, Appl
16	130.6	3.5	3600	US-10-090-827-17	Sequence 17, Appl
17	113	3.0	3057	US-10-090-827-2	Sequence 2, Appl
18	113	3.0	3111	US-10-090-827-3	Sequence 3, Appl
19	113	3.0	3192	US-10-090-827-4	Sequence 4, Appl

ALIGNMENTS

20	113	3.0	3842	US-10-090-827-1	Sequence 1, Appl
21	107.6	2.9	503	US-10-050-786-5	Sequence 5, Appl
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23	59.2	1.6	168	US-09-864-761-27992	Sequence 27992, A
24	53.4	1.4	1614	US-09-976-740-45	Sequence 45, Appl
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42	47.6	1.3	10464	US-09-957-974-1	Sequence 1, Appl
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RESULT 1
US-10-162-012-14
Sequence 14, Application US/10162012
Publication No. US20030051660A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.
APPLICANT: Sltos-Santlago, Inmaculada
APPLICANT: Gu, Wei
TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
FILE REFERENCE: 10448-190001
CURRENT APPLICATION NUMBER: US/10/162,012
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 60/209,845
PRIOR FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: US 09/875,321
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: PCT/US01/18340
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/209,257
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: US 09/875,423
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 3562 ACCGCAAGTGTAGGAGCTGCT 3621
 3719 TGTACTTTTAAATGAT 3770
 3622 TGTACTTTTAAATGAT 3673

RESULT 2
 US-09-875-423-1
 : Sequence 1, Application US/09875423

Patent No. US20020081657A1
 : GENERAL INFORMATION:
 : APPLICANT: Curlys, Rofy A.J.
 : TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL
 : FILE REFERENCE: 10448-059001
 : CURRENT APPLICATION NUMBER: US/09/875,423
 : PRIOR APPLICATION NUMBER: 2001-06-05
 : PRIOR FILING DATE: 2000-06-05
 : NUMBER OF SEQ ID NOS: 6
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 1
 : LENGTH: 3690
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (29)...(3301)

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Db	2122	GGTGGTGGTCCCCCAATTGAAGGATATGGACACAGCTGGCCCTCAACAAATCTGAAGA	2181
QY	2279	TTCTGACAAGGGCGTGGAGTGTGGCTTCCTCGTGACACTGGACGGGGCCCTCCACAAATCA	2338
Db	2182	TTCTGACAAGGGCGTGGAGTGTGGCTTCCTCGTGACACTGGACGGGGCCCTCCACAAATCA	2241
QY	2339	CTCTTTTGTGGGGGCTGAGAGCTCACCAATCAGAGCTTCCTGGAAGCTGGCGACAAGGA	2398
Db	2242	CTCTTTTGTGGGGGCTGAGAGCTCACCAATCAGAGCTTCCTGGAAGCTGGCGACAAGGA	2301
QY	2399	GAACATTTTAAACCGCACACCATTTTCCTCTCTGTACCGAAGAGCGCGTGAAGCATTTCC	2458
Db	2302	GAACATTTTAAACCGCACACCATTTTCCTCTCTGTACCGAAGAGCGCGTGAAGCATTTCC	2361
QY	2459	AGGAGGCTTGCTGCTACTGCTGATCCCATTCAGACACTGGACCGCTCAATTAAGCATTTGGT	2518
Db	2362	AGGAGGCTTGCTGCTACTGCTGATCCCATTCAGACACTGGACCGCTCAATTAAGCATTTGGT	2421
QY	2519	GACAGCAAGTACATCATCCAGCTCTGGATGGAACGGAAATCTCTGTGGGAGCTGT	2578
Db	2422	GACAGCAAGTACATCATCCAGCTCTGGATGGAACGGAAATCTCTGTGGGAGCTGT	2481
QY	2579	AGGCATTCACATGAATCAATTTTTCCTCAAGAGTCTTGACATGCCAGCAGACAGTG	2638
Db	2482	AGGCATTCACATGAATCAATTTTTCCTCAAGAGTCTTGACATGCCAGCAGACAGTG	2541
QY	2639	TGCTTCCCTGGATGGCAATAGCTCCATCAGCTGTGATGATGAGAGCTGTGAATTTACCT	2698
Db	2542	TGCTTCCCTGGATGGCAATAGCTCCATCAGCTGTGATGATGAGAGCTGTGAATTTACCT	2601
QY	2699	CATAGACATTAATGATTTTATTTTGGTGTGGAAGACTACACACAGACTGGAGACTTTT	2758
Db	2602	CATAGACATTAATGATTTTATTTTGGTGTGGAAGACTACACACAGACTGGAGACTTTT	2661
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RESULT 4
US-10-162-012-16
Sequence 16, Application US/10162012
Publication No. US20030051660A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.
APPLICANT: Silos-Santlago, Imaculada
TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
FILE REFERENCE: 10448-190001
CURRENT APPLICATION NUMBER: US/10/162, 012
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 60/209, 845
PRIOR FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: US 09/875, 321
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: PCT/US01/18340
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/209, 257
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: US 09/875, 423
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: PCT/US01/18398
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/209, 238
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: US 09/875, 363
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: PCT/US01/18247
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/227, 068
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 09/928, 530
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: PCT/US01/25475
PRIOR FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: US 60/226, 770
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: US 09/934, 421
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/US01/26096
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/279, 281
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 10/109, 029
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: PCT/US02/09728
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/290, 288
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US (not assigned)
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 3276
TYPE: DNA
ORGANISM: Homo sapiens
US-10-162-012-16

Query Match 85.7%: Score 3229.6; DB 9: Length 3276;
Best Local Similarity 99.4%: Pred. No. 0;
Matches 3257; Conservative 1: Mismatches 0; Indels 18; Gaps 1:

OY 144 ATGGCCGGCCGGGCTCCGCGCGCGCGCTCCGGGGGGCGCTTCCGCTTCCGCTCC 203
DB 1 ATGGCCGGCCGGGCTCCGCGCGCGCGCTCCGGGGGGCGCTTCCGCTTCCGCTCC 60
OY 204 GCGCTTCTACGCGCGCGCGCGCGCGCTTCCGCGCGCGCTTCCGCGCGCTTCC 263
DB 61 GCGCTTCTACGCGCGCGCGCGCGCGCTTCCGCGCGCGCTTCCGCGCGCTTCC 120
OY 264 GTGGTGAAGCTTGGGCGCTGGGCTTGGTGGGAGATAAATTCATTGCTGTAAGTAC 323
DB 121 GTGGTGAAGCTTGGGCGCTGGGCTTGGTGGGAGATAAATTCATTGCTGTAAGTAC 180
OY 324 TCGGCTTCCGAGCTTCTGCAAAAGAAATACAAAGATGAGAAAGACCTTGCCTAGAA 383
DB 181 TCGGCTTCCGAGCTTCTGCAAAAGAAATACAAAGATGAGAAAGACCTTGCCTAGAA 240
OY 384 GAAATGATGCGCTCCCAAGCTGTAAGAAAGCTGGCAAAAGCAATGGAAGATGTTTAC 443
DB 241 GAAATGATGCGCTCCCAAGCTGTAAGAAAGCTGGCAAAAGCAATGGAAGATGTTTAC 300
OY 444 AAGAGCTGAGGCGCTGACAGCGCTTGGTGGAGGCTGACAGAAAGACACCTGAAACAT 503
DB 301 AAGAGCTGAGGCGCTGACAGCGCTTGGTGGAGGCTGACAGAAAGACACCTGAAACAT 360
OY 504 GAATTTGATGACAGCTTACATGATGAAATCTTCAATGCTGCTGATTAATGAAAGGAC 563
DB 361 GAATTTGATGACAGCTTACATGATGAAATCTTCAATGCTGCTGATTAATGAAAGGAC 420
OY 564 AAGAGCGGGAATTTTGGAGCTGGGAAGGAATTCATCTTACCCCAATGACATTTT 623
DB 421 AAGAGCGGGAATTTTGGAGCTGGGAAGGAATTCATCTTACCCCAATGACATTTT 480
OY 624 AATTAATTTGCTGTGAACATCACTTAAGTGAAGCTCAAGTACCAAGCAATGTACAAC 683
DB 481 AATTAATTTGCTGTGAACATCACTTAAGTGAAGCTCAAGTACCAAGCAATGTACAAC 540
OY 684 AAGAGCCCTGCAATTTGTCAATGGGCTTATGCTGTAATCTCTAACAAGTTTTTGA 743
DB 541 AAGAGCCCTGCAATTTGTCAATGGGCTTATGCTGTAATCTCTAACAAGTTTTTGA 600
OY 744 GATTAATTTGACGCTGACCATCTCTCATATGCGAGTACTTTGGAGTGCAGAGGCTTT 803
DB 601 GATTAATTTGACGCTGACCATCTCTCATATGCGAGTACTTTGGAGTGCAGAGGCTTT 660
OY 804 TTTAGGCACTATCCGGGGATTAATGGGAACAGATGAGAAATGAGTCAATGCTTCGAC 863
DB 661 TTTAGGCACTATCCGGGGATTAATGGGAACAGATGAGAAATGAGTCAATGCTTCGAC 720
OY 864 TGCAGAGAACCGAAATGTGATCATCCAGGAGCAACTTCTCCGAAAGCGTGTGATTTTA 923
DB 721 TGCAGAGAACCGAAATGTGATCATCCAGGAGCAACTTCTCCGAAAGCGTGTGATTTTA 780
OY 924 GTTGAAGTGAAGGAGATGAAAGACCTCGCTGACTATGCGGAAGCAAGCTCTA 983
DB 781 GTTGAAGTGAAGGAGATGAAAGACCTCGCTGACTATGCGGAAGCAAGCTCTA 840
OY 984 TCCATTTTGGATACATTTGGGAGTATGACTTCTTCAACATATATGCTTATATGAGAG 1043
DB 841 TCCATTTTGGATACATTTGGGAGTATGACTTCTTCAACATATATGCTTATATGAGAG 900
OY 1044 CTTCACCTATGAGAACCTTGCTGAATGGAACCTTTGTCGACCGGAGCAACAA 1103
DB 901 CTTCACCTATGAGAACCTTGCTGAATGGAACCTTTGTCGACCGGAGCAACAA 960
OY 1104 GAGCACTTCAAGGAGCATCTGACAAACTTTTCCGCAAGGAATTTGGAATGATATA 1163
DB 961 GAGCACTTCAAGGAGCATCTGACAAACTTTTCCGCAAGGAATTTGGAATGATATA 1020

OY 1164 GCTCTGAATGAGGCTTCAACATCTGAGTGAATTTCAACACAGGAGCAAGATATC 1223
DB 1021 GCTCTGAATGAGGCTTCAACATCTGAGTGAATTTCAACACAGGAGCAAGATATC 1080
OY 1224 TGCAGTACGAGCATATGCTCATTAATGATGAGGCGGTGAGACACTTATACAAATCTTT 1283
DB 1081 TGCAGTACGAGCATATGCTCATTAATGATGAGGCGGTGAGACACTTATACAAATCTTT 1140
OY 1284 GCAAAATACAAATTTGGCCAGATTCGAAAGCTTGCATCTTCAATACCTCATTTGAGCAG 1343
DB 1141 GCAAAATACAAATTTGGCCAGATTCGAAAGCTTGCATCTTCAATACCTCATTTGAGCAG 1200
OY 1344 GCTGCGTTTGCAGACATTTAAAGTGAATGGCCGTGCGCAACAAAGATTTTACCAG 1403
DB 1201 GCTGCGTTTGCAGACATTTAAAGTGAATGGCCGTGCGCAACAAAGATTTTACCAG 1260
OY 1404 ATCTCCACTTGGCTGATGTCGAGAGAAATGTGATGGAATACCTTACGCTTACCGG 1463
DB 1261 ATCTCCACTTGGCTGATGTCGAGAGAAATGTGATGGAATACCTTACGCTTACCGG 1320
OY 1464 CCCAAAGTCATCGACACGAGCATGATGTGTGACCGAGCAAGCTTACATTTGACAGCACT 1523
DB 1321 CCCAAAGTCATCGACACGAGCATGATGTGTGACCGAGCAAGCTTACATTTGACAGCACT 1380
OY 1524 -----CTGACTGATGATCAGGCGCCGCTGATGATGACCACTGATGCC 1565
DB 1381 CTCTCCACGAGCAAAAGCTGACTGATGATCAGGCGCCGCTGATGATGACCACTGATGCC 1440
OY 1566 ATGCTGTGTTTGAATGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1625
DB 1441 ATGCTGTGTTTGAATGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1500
OY 1626 GGCAGAGATGTCCCACTGAAGAACTTCTGAGAACATCCCAATACAAGTTAGGGAAT 1685
DB 1501 GGCAGAGATGTCCCACTGAAGAACTTCTGAGAACATCCCAATACAAGTTAGGGAAT 1560
OY 1686 CACGGTTATGCTTGCATACCAATTAATGATGATGATGATGATGATGATGATGATGAT 1745
DB 1561 CACGGTTATGCTTGCATACCAATTAATGATGATGATGATGATGATGATGATGATGATG 1620
OY 1746 CTGCTGTAGCAAGAAAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1805
DB 1621 CTGCTGTAGCAAGAAAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1680
OY 1806 GAGGTGAGTGGGAGACCGAGATGACGTGTGAGAAATGCTATGCTGATGAGAAAGAG 1865
DB 1681 GAGGTGAGTGGGAGACCGAGATGACGTGTGAGAAATGCTATGCTGATGAGAAAGAG 1740
OY 1866 GGGAGTTTTCATGAGAGTGAAGAGACAGTGGCAAGGGAACGGTTTTTGGTGAATG 1925
DB 1741 GGGAGTTTTCATGAGAGTGAAGAGACAGTGGCAAGGGAACGGTTTTTGGTGAATG 1800
OY 1926 ACAAAATGACTATTAATACAGACATCAAGGGTACTCTTGAATTTAGTTAGTGGCGCTT 1985
DB 1801 ACAAAATGACTATTAATACAGACATCAAGGGTACTCTTGAATTTAGTTAGTGGCGCTT 1860
OY 1986 TCCAGAGTCAATGGGAATATTTCTTCCGAGGGAATGTAAACCATGGAAGAGCGCTGAT 2045
DB 1861 TCCAGAGTCAATGGGAATATTTCTTCCGAGGGAATGTAAACCATGGAAGAGCGCTGAT 1920
OY 2046 GACTTAGAATCCGAGTGTCTTGGAGATGAAATGGTCTACTGCAACCTAAGCTA 2105
DB 1921 GACTTAGAATCCGAGTGTCTTGGAGATGAAATGGTCTACTGCAACCTAAGCTA 1980
OY 2106 CACCTGAGCACCGCATCTGCTCAGTTAGAGGATTAAGCTTACCTTAAAGCAAA 2165
DB 1981 CACCTGAGCACCGCATCTGCTCAGTTAGAGGATTAAGCTTACCTTAAAGCAAA 2040
OY 2166 GAACTTGTGCTCAGTGTGATTAAGAAATTTGATCAAGAAGTCTTTTGGAGCGGCTGGTG 2225
DB 2041 GAACTTGTGCTCAGTGTGATTAAGAAATTTGATCAAGAAGTCTTTTGGAGCGGCTGGTG 2100
OY 2226 AGTCCCCCATTTGAAGGATTTGAGACAGCTGCGCTCAACCAATCTGAATAATTTCTGAC 2285

Db 2101 AGTGGCCCACTGTAAGGATTTGGACAGCTTGCCCTCAACAAATCTGAAAATTTCTGAC 2160
OY 2286 AAGGGCGTGGAGGTTGCTCTCTCGGACACTCGACGGGCTCTCCAGAAATCAACCTGTTT 2345
Db 2161 AAGGGGCTGGAGGTTGCTCTCTCGGACACTCGACGGGCTCTCCAGAAATCAACCTGTTT 2220
OY 2346 GTGCGGGCTGAGCAGCTCAACCAATGAGACTTCTGAAAAGCTGGCGACAAGGAACATT 2405
Db 2221 GTGCGGGCTGAGCAGCTCAACCAATGAGACTTCTGAAAAGCTGGCGACAAGGAACATT 2280
OY 2406 TTATAAGCAGACACTTCT 2465
Db 2281 TTATAAGCAGACACTTCT 2340
OY 2466 TTGCTGTAATCTGATCCATTCACACTGACAGCAGTCAATATAAGCAATGCTGAGACGA 2525
Db 2341 TTGCTGTAATCTGATCCATTCACACTGACAGCAGTCAATATAAGCAATGCTGAGACGA 2400
OY 2526 AGTACATCCATCCAGCTCTGATGAGAGGAAATCTCTGTGTGGCAGCTTAGGCATT 2585
Db 2401 AGTACATCCATCCAGCTCTGATGAGAGGAAATCTCTGTGTGGCAGCTTAGGCATT 2460
OY 2586 CAGATTAACCTGTAATTTTCCAAAGAGTTTGTGACTGCGCAGCAGACAGTGTCTCC 2645
Db 2461 CAGATTAACCTGTAATTTTCCAAAGAGTTTGTGACTGCGCAGCAGACAGTGTCTCC 2520
OY 2646 CTGATGAGCAATGCTCCATCCAGCTGATGAGAGCTGTAATGTAACCTCATAGAC 2705
Db 2521 CTGATGAGCAATGCTCCATCCAGCTGATGAGAGCTGTAATGTAACCTCATAGAC 2580
OY 2706 AATTAATGATTTATTTTGTGTCTGTAAGACTACACAGACTGAGACTTTTGTGTGAG 2765
Db 2581 AATTAATGATTTATTTTGTGTCTGTAAGACTACACAGACTGAGACTTTTGTGTGAG 2640
OY 2766 ATCGAGGAGGCTGTGATGAACAAATGCTAACAATGGCTCTTTAAAGAAATTAACCTT 2825
Db 2641 ATCGAGGAGGCTGTGATGAACAAATGCTAACAATGGCTCTTTAAAGAAATTAACCTT 2700
OY 2826 TATGACTACCAAGCCATGTGTAGAGCCACAAGAGAGGAGGAGGAGGAGGAGGAGGAGG 2885
Db 2701 TATGACTACCAAGCCATGTGTAGAGCCACAAGAGAGGAGGAGGAGGAGGAGGAGGAGG 2760
OY 2886 CTGATCTCTTATTAATGCT 2945
Db 2761 CTGATCTCTTATTAATGCT 2820
OY 2946 TTCTCTGTGTGATTTAATCT 3005
Db 2821 TTCTCTGTGTGATTTAATCT 2880
OY 3006 AAATTTGAACACAGCCCTGAGGCTGTGTACTGAAATATCCAGCAATGCTCTCTCTCTCT 3065
Db 2881 AAATTTGAACACAGCCCTGAGGCTGTGTACTGAAATATCCAGCAATGCTCTCTCTCTCT 2940
OY 3066 ACCATCAAGGAGACTACAGGGAATATGCTGTGTAAGACTGCTCAAGTCTTTGTGATC 3125
Db 2941 ACCATCAAGGAGACTACAGGGAATATGCTGTGTAAGACTGCTCAAGTCTTTGTGATC 3000
OY 3126 CAGCAAAATCCCAAGCAGCAACTGTTCAATGTTGTGTGTGAGCAGCAGCTGCTGTGAA 3185
Db 3001 CAGCAAAATCCCAAGCAGCAACTGTTCAATGTTGTGTGTGAGCAGCAGCTGCTGTGAA 3060
OY 3186 TCTGTGGGCCCCCATCAGCATGGCAGCCCAATGAAATCAGATTAATGAAATCCCTTAAGTGT 3245
Db 3061 TCTGTGGGCCCCCATCAGCATGGCAGCCCAATGAAATCAGATTAATGAAATCCCTTAAGTGT 3120
OY 3246 GAACGCTTAAGAGGCCAGAAATGAGAGGCGCCCAAGATCTTGTGATGAGCTTCCATCCT 3305
Db 3121 GAACGCTTAAGAGGCCAGAAATGAGAGGCGCCCAAGATCTTGTGATGAGCTTCCATCCT 3180
OY 3306 GAGGAGATGCAAGGAGTGTGTGGGTGCGCGAGTCTTCAAGCCAGACAGCTCTCTCT 3365

Db 3181 GAGGAGAAATCAAGGAGTGTGGGGTGCCGCCAGTCTCCAAAGCCAGACAGTCTCTT 3240
OY 3366 CTGCTCCCTCTGCTTTTGATGCTCTCTCTCAAGGGA 3401
Db 3241 CTGCTCCCTCTGCTTTTGATGCTCTCTCAAGGTGA 3276
RESULT 5
US-09-875-423-3
; Sequence 3. Application US/09875423
; Patent No. US20020081657A1
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Roy A. J.
; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL
; FILE REFERENCE: 10448-059001
; CURRENT APPLICATION NUMBER: US/09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR FILING DATE: 2000-06-05
; NUMBER OF SEQ. ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ. ID NO 3
; LENGTH: 3276
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-423-3
Query Match 85.7%; Score 3229.6; DB 10; Length 3276;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 3257; Conservative 1; Mismatches 0; Indels 18; Gaps 1;
OY 144 ATGGCGGGCGGGGCTCG 203
Db 1 ATGGCGGGCGGGGCTCG 60
OY 204 GCGCTTCTACG 263
Db 61 GCGCTTCTACG 120
OY 264 GTGTGAGCTCTGGGCGCTCGGCTTTTGTGTGGGAGATTAATTCATGCTGTAAGTAC 323
Db 121 GTGTGAGCTCTGGGCGCTCGGCTTTTGTGTGGGAGATTAATTCATGCTGTAAGTAC 180
OY 324 TCGGTTCCAGCTTCTGCAAAAGAAATACAAAGATATGAGAAACGTTGGCATAGAA 383
Db 181 TCGGTTCCAGCTTCTGCAAAAGAAATACAAAGATATGAGAAACGTTGGCATAGAA 240
OY 384 GAAATGATGGCTCCCACTGGTAAAGAGCTGGCAAGACATGGAAGATGTTTAC 443
Db 241 GAAATGATGGCTCCCACTGGTAAAGAGCTGGCAAGACATGGAAGATGTTTAC 300
OY 444 AAGAACTGTAGGCGCTCAGGCGCTGTGTGAGGCTGCAAGAGAACACACCTGAAACAT 503
Db 301 AAGAACTGTAGGCGCTCAGGCGCTGTGTGAGGCTGCAAGAGAACACACCTGAAACAT 360
OY 504 GAATTTGATGAGACTTAAGATATGATATCTTCAATGCTGTGTGTAATGAAAGGAC 563
Db 361 GAATTTGATGAGACTTAAGATATGATATCTTCAATGCTGTGTGTAATGAAAGGAC 420
OY 564 AAGAGCGGAATTTTGTGAGCTGGGAAAGGAATTCATGTTAGCCCAATGACATTTT 623
Db 421 AAGAGCGGAATTTTGTGAGCTGGGAAAGGAATTCATGTTAGCCCAATGACATTTT 480
OY 624 AATTAATTTGCTGTGAACATCAGTCTAAGTGAAGTCCAAAGTACCAAGCAATGTACAAAC 683
Db 481 AATTAATTTGCTGTGAACATCAGTCTAAGTGAAGTCCAAAGTACCAAGCAATGTACAAAC 540
OY 684 AAGAGCCCTGCAATGCTCAATGGGTTTATTTGCTGAAATCTCTAACAAGATTTTGTGA 743
Db 541 AAGAGCCCTGCAATGCTCAATGGGTTTATTTGCTGAAATCTCTAACAAGATTTTGTGA 600
OY 744 GATAACTTTGACCGTACCATCTCTCATATGCGAGTACTTGTGAAGTGAAGGAGCTTT 803

Query Match	11.1%	Score 419;	DB 10;	Length 519;
Best Local Similarity	100.0%;	Pred. No. 3.1e-109;		
Matches 419; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0
QY 688	ACCCGTCGCAATTTTCATGCGGCTTATTGTCGTGCAATCTCAAAACAAGCTTTTGATAGATA	747		
DB 1	ACCCGTCGCAATTTTCATGCGGCTTATTGTCGTGCAATCTCAAAACAAGCTTTTGATAGATA	60		
QY 748	ACCTTGACCGGACCACTCTCATATGCGAGTACTTTGGAAGTCAAAAGCGCTTTTATA	807		
DB 61	ACCTTGACCGGACCACTCTCATATGCGAGTACTTTGGAAGTCAAAAGCGCTTTTATA	120		

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? PRIOR FILING DATE: 2001-07-13
? PRIOR APPLICATION NUMBER: US 60/302,277
? PRIOR FILING DATE: 2001-06-29
? PRIOR APPLICATION NUMBER: US 60/298,698
? PRIOR FILING DATE: 2001-06-15
? PRIOR APPLICATION NUMBER: US 60/293,574
? PRIOR FILING DATE: 2001-05-25
? NUMBER OF SEQ ID NOS: 112
? SOFTWARE: Jpatent
? SEQ ID NO: 99
? LENGTH: 667
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: 5'UTR
? LOCATION: 1..94
? NAME/KEY: CDS
? LOCATION: 95..613
? NAME/KEY: 3'UTR
? LOCATION: 614..667
? NAME/KEY: polyA_signal
? LOCATION: 636..641
? NAME/KEY: polyA_site
? LOCATION: 652..667
? US-09-924-340-99

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Query Match	10.3%	Score 387.2	DB 9	Length 667
Best Local Similarity	96.3%	Pred. No. 4.6e-100		
Matches 395	Conservative 1	Mismatches 14	Indels 0	Gaps 0
QY	1508	TTACATTACAGCACTCTGACTGATGATCAGGGCCCGCTCGTATGACCACTGATACCAT	1567	
Ddb	157	TTTCTCTTCCATCCAGCTGACTGATGATCAGGGCCCGCTCGTATGACCACTGATACCAT	216	
QY	1568	GCCTGTGTTTGTAGCAGCAAGCAACAGATCGAAGGCAATCTCTCTGGAGTGGTTGG	1627	
Ddb	217	GCCTGTGTTTGTAGCAGCAAGCAACAGATCGAAGGCAATCTCTCTGGAGTGGTTGG	276	
QY	1628	CACAGATGTCCCAATGGAAGAACTTCTGAGACCATCCCAATATACAAGTTAGGGATTCA	1687	

Db 277 CACAGATGTCCAGTGAAGAACTTCTGAAGACCATCCCAATAACAGTTAGGAGATTCA 336
OY 1688 CGGTATGCGCTTTCAGTACAAATAATGRTATATCTGTACGCATCCGGAGCTCAGGCT 1747
Db 337 CGGTATGCGCTTTCAGTACAAATAATGRTATATCTGTACGCATCCGGAGCTCAGGCT 396
OY 1748 GCTGTACGAGAGAGAAAAAGCAGAGAACTAATGATAGTACGCTCTCTCTGA 1807
Db 397 GCTGTACGAGAGAGAAAAAGCAGAGAACTAATGATAGTACGCTCTCTCTGA 456
OY 1808 GGTGAGTGGAGAGACCGAGATGACGTGTGAGAAATGCTATGCTGAATCGAAGACGGG 1867
Db 457 GGTGAGTGGAGAGACCGAGATGACGTGTGAGAAATGCTATGCTGAATCGAAGACGGG 516
OY 1868 GAATTTTCCATGGAGGTGAAGACAGTGCAGAAAGGAGCGGTTT 1917
Db 517 GAATTTTCCATGGAGGTGAAGACAGTGCAGAAAGGGGTACATTTT 566

RESULT 8

US-09-992-600A-99
; Sequence 99, Application US/09992600A
; Publication No. US20030027161A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephanie
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US4.DIV
; CURRENT APPLICATION NUMBER: US/09/992,600A
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Jpatent
; SEQ ID NO 99
; LENGTH: 667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..94
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 95..613
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 614..667
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 636..641
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 652..667
US-09-992-600A-99

Query Match 10.3%; Score 387.2; DB 9; Length 667;
Best Local Similarity 96.3%; Pred. No. 4,6e-100;
Matches 395; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

OY 1508 TTACATTTGACACACTCTACATGATGATAGGCGCCGCTCTGATGACCACTGTAGCCAT 1567
Db 157 TTTCCTCTCCATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 216

OY 1568 GCTGTGTGTAGTAAAGCAAGCAACCAATGATGAGGCAATTTCTTGGAGTGTGG 1627
Db 217 GCTGTGTGTAGTAAAGCAAGCAACCAATGATGAGGCAATTTCTTGGAGTGTGG 276
OY 1628 CACAGATGTCCAGTGAAGAACTTCTGAAGACCATCCCAATAACAGTTAGGAGATTCA 1687
Db 277 CACAGATGTCCAGTGAAGAACTTCTGAAGACCATCCCAATAACAGTTAGGAGATTCA 336
OY 1688 CGGTATGCGCTTTCAGTACAAATAATGRTATATCTGTACGCATCCGGAGCTCAGGCT 1747
Db 337 CGGTATGCGCTTTCAGTACAAATAATGRTATATCTGTACGCATCCGGAGCTCAGGCT 396
OY 1748 GCTGTACGAGAGAGAAAAAGCAGAGAACTAATGATAGTACGCTCTCTCTGA 1807
Db 397 GCTGTACGAGAGAGAAAAAGCAGAGAACTAATGATAGTACGCTCTCTCTGA 456
OY 1808 GGTGAGTGGAGAGACCGAGATGACGTGTGAGAAATGCTATGCTGAATCGAAGACGGG 1867
Db 457 GGTGAGTGGAGAGACCGAGATGACGTGTGAGAAATGCTATGCTGAATCGAAGACGGG 516
OY 1868 GAATTTTCCATGGAGGTGAAGACAGTGCAGAAAGGAGCGGTTT 1917
Db 517 GAATTTTCCATGGAGGTGAAGACAGTGCAGAAAGGGGTACATTTT 566

RESULT 9

US-10-116-949-1
; Sequence 1, Application US/10116949
; Publication No. US20030044911A1
; GENERAL INFORMATION:
; APPLICANT: Lerman, Michael I.
; APPLICANT: Minna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Boning
; APPLICANT: Duh, Fuh-Mei
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
; FILE REFERENCE: NIH-05043
; CURRENT APPLICATION NUMBER: US/10/116,949
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/470,443
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/114,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 5463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (162)..(3599)
US-10-116-949-1

Query Match 5.7%; Score 214; DB 9; Length 5463;
Best Local Similarity 47.3%; Pred. No. 6.9e-50;
Matches 845; Conservative 0; Mismatches 900; Indels 41; Gaps 5;

OY 61 GGGCTGCGCCACCGCCGCTCCGCGAGTCCCGCGCGCTCTGCTGCGCGCGCAC 120
Db 165 GCGGTGCGCGCTCGGACCTGCGCGCTCTGCGCGCGCGCGCGCGCGCGCGCC 224
OY 121 GGGCGCTGCGAGAGCCACGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db 225 TGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 284
OY 181 GGGCTGCGCGCTCTGCGCTGCGCGCGCTCTGCGCGCGCGCGCGCGCGCGCT 240
Db 285 GCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCGCGCGCGCGCG 344
OY 241 CGGACGACGAGATACCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300


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Db 345 TACAGCTTC--CCCCACAGCACACGATGACAGCTGGGCCCGCGCTCGGAGCAGAGG 402
QY 301 TAAATTCATTTGCTGTAAGTACTCCGGTTCCAGCTTTCGCAAAAGAAATACAAAGT 360
Db 403 TCGAGCGCGTGAATGCGGATTTTGGAGGCGTCCGACAGCTCGTGAAGATTCACAGACA 462
QY 361 ATGAGAAAGAGTGGCCATAGAAATTTGATGGCTCCAACTGGTAA/GAAGCTGGCAA 420
Db 463 ACCGGAACCTGTTCGAGTACAGAGAAATAGGCTCAGAAAGTTGGTGAAGAGTGGCAG 522
QY 421 AGAATATGAGAGATGTTTTCACAGAAATCTGAGGCGTTCAGGCTGTGGTGGAGCTG 480
Db 523 GGGACATTTGAGAGCTTCTTGACAGAAAGTGGAGCGCTGAAAGAGACTGGCTGATCTG 582
QY 481 CAGAAAGACACACCTGAAACATGAAATTTGATGACAGCTTACGATATGATCTT----- 535
Db 583 CAGAGAACTTCCAGAAAGCACACCGCTGGCAGAGACACATCAAGAGAGAGACATCGTGT 642
QY 536 -----CMAATGCTGTGCTGATMAATGAAAGGACAAAGCGGGAAT 576
Db 643 ACTATGACGCCAAGGCTGACGCTGAGCTGAGACCCCTGAGATGAGATGTGGAAAGG 702
QY 577 TTTTGGAGCTGGGAAAGAAATTCATCTTACGCCCAATGACCAATTTTAAATTTGGCTG 636
Db 703 GGTCTAAGGCCACACCCCTAAGGCTGACTTCATCGAGAGCCCAACCTTCAAGAACAG 762
QY 637 TGAACATCAAGTCAAGTACAGTCCAGTACCAAGCAACATGTACAAACAGACCTGCAA 696
Db 763 TCAACTATTCATACGCGGCTGTACAGATCCCTAAGGACATCTCAAAAGGCTCCACGTCA 822
QY 697 TTGTCAATGGGGTTTATTTGCTGAACTCTTAAACAAAGTTTGTGATTAATCTTGAC 756
Db 823 TCCCTCAATGAGCTCAACTGACAGAGAGCCCTGAGAAATGTGTTCAATGGAACCCGAGAC 882
QY 757 GTGACCCATCTCTCATATGCGCAGTACTTGGAAAGTGCAAAGGCTTTTGTAGGCACTATC 816
Db 883 AAGACCCCACTGTGTGTGGAGTCTTTCGGCAGCGCCACAGAGAGTCACTCGCTACTAC 942
QY 817 CGGGGATTTAAATGGGAAACAGATGAAATGAAATGATCTTCCCTTCGACTCAGAACCGAA 876
Db 943 CGGCCACCCCGTGGGAGGAGCCCAAGAAAGATGACCTGTACATGTCCCAAGGA--GAC 999
QY 877 AATGTACATCCAGGAGCAGCACTTCCGAAAGAGTGTGATTTTGTGAGTGCAGTG 936
Db 1000 CTTGATATATCCAGGGGCGCTGTCACCCAAAGATATGTCATCGT3GATGTGAGTG 1059
QY 937 GCAGATGAAGAGACTCCGCTGACTATGCGAAGCAAAACAGTCTCATCCATTTTGGATA 996
Db 1060 GCAGTGTAGGGGCTGACCCCTGAGCTGATGAAAGACATCTGTGCGCA3ATGCTGGACA 1119
QY 997 CACTTGGGAGTATGACTTCTTCAACATATTTGTTAATAGAGAGCTTCACTATGTGG 1056
Db 1120 CGCTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1179
QY 1057 AACCTTGGCTGAATGAACTTTGTTGTCAGCGCAGCAGGACAAACAAAG3CACTTCAGGG 1116
Db 1180 CATGCTTACACACC-----TGGTGAAGGCCAATGTGCGCAACAAAG3GTGTTCAAGG 1233
QY 1117 AGCATCTGAGCAAACTTTTGGCCAAAGAAATTTGAATGTTGATTTACCTTGAATGAGG 1176
Db 1234 AAGCTGTGACAGGATGTTGGCCAAAGGACCAACAGGCTTACAAAGCCGG3TTTGATATG 1293
QY 1177 CCTTCAACATTTCTGATGATTTTCAACACAGGACAGGAAAGATCTG3AGTACAGGCCA 1236
Db 1294 CTTTGAACAGCTGACAGATCCAAACATCACTCGGGCC-----AAGTG3AACAAGATGA 1347
QY 1237 TCATGCTCATTAAGTATGAGGCGGTGACACCTATGATATCAATCTTTTCAAAATATAT 1296
Db 1348 TCATGATGTTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1407
QY 1297 GCGCAGATTCGAAGAGTGTGCTTTCATATACATCAATTTGAGCAGAGAGCC3GCTTTGAG 1356

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Db 1408 GGCCAAACCGGAGGCTGGCGCTGTTTACTTCTCCGTGGGACATATATATGACTCA 1467
QY 1357 ACAATCTAAAGTGAATGCGCTGTGTCACAAAGAGATTTTATACCAGATCTCACTTGG 1416
Db 1468 CACCGCTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1527
QY 1417 CTGATGTGACAGGAAATGTATGATATGATATCTTCACTGCTTACGCGGCCCAAGTCA 1476
Db 1528 GAGCATTCGCCATCAACACAGAGAAATATGATGATGATGATGATGATGATGATGATGAT 1587
QY 1477 ACCAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1536
Db 1588 CAGGCAAGAGGAGGCCACAGAGTTCAGTGGACCAACGTTTATGAGATGACCTGGAGCTG 1647
QY 1537 AGGGCCCGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1596
Db 1648 GGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1707
QY 1597 GATGAGAGGAGCATTTCTTCTGAGAGTGTGGACACATGTCCTGTTTATGACAGAGAA 1656
Db 1708 AGAAGAAACAGCTGATTCCTTGGGCTGATGGGCAATGAGCTGCTGAATGATCAAGA 1767
QY 1657 AGACCATCCCAATATCAAGTATGAGGATTCACGCTTATGCTTTCATATCAATATATG 1716
Db 1768 GGTGACCCCAACTATACAGCTTGGAGCCCAAGGCTATGTTTGCATGACCTGAAAG 1827
QY 1717 GRTATATCTGACGATCCGGAATCAGGCTGCTGTACGAAGAAAGAAAGCAAGAA 1776
Db 1828 GCTAGGTTGTGCTGACACCCCAATCTCAAGCCCAAGACCAACCACTCCGGAGACCTGTGA 1887
QY 1777 AACCTACTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1822
Db 1888 CTCTGAGACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1933

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RESULT 10
US-10-116-949-3
Sequence 3, Application US/10116949
Publication NO. US20030044911A1
GENERAL INFORMATION:
APPLICANT: Lerman, Michael I.
APPLICANT: Minna, John D.
APPLICANT: Latif, Farida
APPLICANT: Wei, Ming-Hui
APPLICANT: Sekido, Yoshitaka
APPLICANT: Gao, Boning
APPLICANT: Duh, Fuh-Mei
TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
FILE REFERENCE: NIH-05043
CURRENT APPLICATION NUMBER: US/10/116,949
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/470,443
PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/114,359
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 3
LENGTH: 5482
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (181)...(3618)
US-10-116-949-3

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Query Match 5.7%; Score 214; DB 9; Length 5482;
Best Local Similarity 47.3%; Pred. No. 6.9e-50;
Matches 845; Conservative 0; Mismatches 900; Indels 41; Gaps 5;
QY 61 GCGCTCGGCCACCGCCGCTCCGCGGACGCTCCGCGGCGCGCTCTCGTCCGCGCGGACG 120
Db 184 GCGGTGCGGCTCGGACCTGGCGGCGCTCTGCGCCGCGCCAGCGGAGTGCAGCGCC 243

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LOCATION: (185) . (3415)
US-10-116-949-5

Query Match 5.5%; Score 206.4; DB 9; Length 5279;
Best Local Similarity 47.9%; Pred. No. 1e-47;
Matches 757; Conservative 0; Mismatches 786; Indels 39; Gaps 4;

265 TGGTGAAGCTCTGGCCCTGGCTTTTGTGGGAGATTAATTCATTGCTGTCACTACT 324
183 TATGTCAGACGATGGGCGCGCTCTGGACAGAGAGCTCACGGCGATGCGGATTTTGG 242
325 CCGGTTCCAGCTCTTGGCAAAAGAAATACAAAGATATAGAAAGACGTTGCCATGAAG 384
243 GAGGGCTCCAGAGCTCCCTGAGATTTCAGAGACAAACCGGAACTGTTGAGATACAG 302
385 AATTGATGGCTCCCAACGTTAAAGAGTAAAGACCTGGCAAAAGAAATGGAAGATCTTCA 444
303 AGAATGAGCTTGAAGAGTTGGTGGAGAGAGTGGCAGGGGACATGAGACCTTCTGGACA 362
445 AGAGCTGAGGCGCTGACGCGCTGTGGAGGCTGCAGAGAGACACACTGAAACATG 504
363 GGAAGGTGACGCGCTGAAAGAGACTGGCTGATGCTGACAGAACTTCCAAAGACACCC 422
505 AATTGATGCAACACTTACAGTATGAATCTTCAA-----TG 540
423 GCTGCGAGACAACATCAAGAGAGAACATGCTGATGATGACGCCAAAGCTGACGCTG 482
541 CTGCTCTGATTAATGAAGAGGACAAAGAGGGAATTTTGGAGCTGGGAAAGATTTCA 600
483 AGCTGAGAGACCTTGAAGATGAGATGAGTGGAAAGGGGCTGTAAGGCCACCTTAAGGC 542
601 TCTTGAAGCCCAATGACATTTTAAATTTTGCCTGTGACATCAGTCAAGTGAAGCTCC 660
543 TGGACTTATCGAGAGACCAAACTTCAAGAACAGTGAACATTAATCATAGGGGCTGAC 602
661 AAGTCCAAACCAACATGTAACAACAAGACCTGCAATTTGCAATGGGCTTATGCTGTG 720
603 AGATCCCTACGACATCTCAAAAGGCTCCACCTGATCCTCAATGAGCTCAACTGAGAC 662
721 AATCTCTAAACAAAGTTTGTAGATTAATTTGACCTGAGGACCATCTCTAATGAGCAT 780
663 AGGCTCTGAGAGATGTGTCATGGAACACCGACAAAGACCCCACTGCTGTGGCAGG 722
781 ACTTGAAGTGAAGGCGCTTTTGAAGCATATCGGGGATTAATGAGCAAGATG 840
723 TCTTGGGAGGCGCACAGAGTACTGCTACTACCGGCCACCCCGTGGAGGCCCA 782
841 AGATGAGGATGCTGCTTGCACATGCAAGAACCGAAATGATACATCAAGCAGCACTT 900
783 AGAAGATGACCTGTACATGCTCCGAAGGA---GACCTGTATATTCAGAGGGGCTGCT 839
901 CTCCGAAGAGCTGTATTTAGTTCGCTGATGAGAGAGAGATGAAAGATCCCTCTGA 960
840 CACCCAAAGACATGTCTATCGTGGATGAGATGAGTGGCAGTGGAGCGGCTGACCCCTGA 899
961 CTATGCGAAGCAAAAGCTCATCATTTTGAATACACTTGGGGATGAAGATCTTCTCA 1020
900 AGCTGATGAAGACATGTGTGTCGAGATGCTGACACCCCTGTCTGATGAAGACATGTA 959
1021 ACATTAATGCTTAAATGAGAGAGCTTCACTATGGAACCTTGGCTGAAGAGAACTTGG 1080
960 ATGTGGCTGCTTCAAGAGAGGACAGAGCTGTGATGCTTACACACAC-----TGG 1013
1081 TGCAGGCGAGAGCAAAAGAGAGCTTCAAGGAGACATCTGGACAACTTTTCCGCA 1140
1014 TGCAGGCGCATGTGCGCAACAAGAGGTGTTCAAGAGAGCTGTCAAGGCAATGCTGGCA 1073
1141 AAGCAATTTGAATGTTGATATAGCTCTGAATGAGGCTTCAACATCTCTAGTATTCA 1200
1074 AGGCAACCAAGAGCTTACAGGCGGCTTTGAGTATGCTTTGACAGACTTCAGAACTCCA 1133
1201 ACCAAGCGGACAAAGAGATGTGCAAGGCAATGCTCATATACATGATGGGCGG 1260

DB 1134 ACATCAC-----TCGGGCCCACTGCAACAAGATGATGATGTTCCAGGATGTGTG 1187
QY 1261 TGGACACCTATGATFACATTTTGGCAAAATFACATTTGGCCAGATTCGAAGGTTCCATCT 1320
DB 1188 AGGACCGCGTGCAGAGAGCTTTTGAAGATGATGATGAGCCAAACCGAGCGTCCGGTGT 1247
QY 1321 TCACATACCTCATTTGACGAGGAGTGGCTTTCAGACCAATCTAAAGTGGATGGCTGTG 1380
DB 1248 TTTACTTTCCGTTGGGCGCAGCATTAATGATGATGATGATGATGATGATGATGATG 1307
QY 1381 CCAACAAGAGATTTTAAACAGATCTCCACCTTGGCTGATGATGATGATGATGATGATG 1440
DB 1308 CCAACAAGAGCTTCTATTTTGAATGATGATGATGATGATGATGATGATGATGATGATG 1367
QY 1441 AATACCTTACGCTTACGCGGCCCAAAAGTCAATGACAGAGAGATGATGATGATGATG 1500
DB 1368 AATATCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1427
QY 1501 CCAAGCTTACATTTGACAGACCTGATGATGATGATGATGATGATGATGATGATGATGATG 1560
DB 1428 AGTGAACCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1487
QY 1561 TACCATGCTGTGTTTAAAGACAGAGAGAAACAGATGAAAGGCGATTTCTTGGAG 1620
DB 1488 CTGTTTCAACCTGACACAGATGAGCTTGGGGAAGAAAGAAAGCAAGCTGATCTGGCG 1547
QY 1621 TGGTTGGCAGATGCTCCAGTGAAGAACTTGTGAAGACATCCCAATACAACTTAG 1680
DB 1548 TATGAGGCAATGACGCTGCTGAATGATGATGATGATGATGATGATGATGATGATG 1607
QY 1681 GATTCAGGTTATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
DB 1608 GAGCAACGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1667
QY 1741 TCAGGCTGCTGACGAAGAGAAAGAAAGCAAGAACTTAACTAATFATGATGATGATG 1800
DB 1668 TCAAGCCCAAGACCAACCACTTCCGGGACCTGTGATGATGATGATGATGATGATG 1727
QY 1801 TCTTGAAGTGAAGTGGAGAGA 1822
DB 1728 TAGAGATGAGAAACAAGAGAGA 1749

RESULT 12
US-10-050-786-4
Sequence 4, Application US/10050786
Patent No. US2002015539A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Calcium Channel Polynucleotides, Polypeptides, and Antibodies
FILE REFERENCE: PTO13P1C1
CURRENT APPLICATION NUMBER: US/10/050,786
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 09/774,028
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: PCT/US00/20392
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/145,958
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US 60/149,446
PRIOR FILING DATE: 1999-08-18
PRIOR APPLICATION NUMBER: US 60/189,064
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 4
LENGTH: 1217
TYPE: DNA
ORGANISM: Homo sapiens
US-10-050-786-4
Query Match 3.6%; Score 135.4; DB 9; Length 1217;
Best Local Similarity 99.3%; Pred. No. 7.4e-28;

OY	346	ACAAATATCAAGAGATATGAGAAAGACGTTGGCATAGAAAGAAATTTGATGCCCTCCCACTGG	405
OY	346	ACAAATATCAAGAGATATGAGAAAGACGTTGGCATAGAAAGAAATTTGATGCCCTCCCACTGG	405
Db	176	AATATTATGAGAAATATCAACATTTGTAATCTGTGTGACCAACCAATTAATGACCGCCACTGG	235
OY	406	TAAAGACGTGGCAAAAGACATGAGAAAGATGTTTACAAAGAGCTGAGCGCGTGAAGC	465
Db	236	TGAAATTTGCAAGCCAGGGATTTGAGAACTTCTGAGCAACACATCTTAAAGCCCTGTGA	295
OY	466	GTCTG-----GTGAGGCTGCAGAGAAAGCACACTGAAACATGATTTGATGACG	516
Db	296	GCCCTGCATTTGGAAGCGAGAAATCTCAAGAGCTCACAGTGGAGAGAAATTTTGCA	355
OY	517	ACTTCACATATGAACTACTTCAATCTGCTGCTGTAATTAATGAAAGGACAAAGCGGAAT	576
Db	356	GCAATGAAGTTGTCATCTACATCCAAAGATGATCTCGATCTCGAAGAAATTAAGACATG	415
OY	577	TTTTCGACCTGGAAAGAAATTCATCTTACCCCAATGACCAATTTAATTTGCTTG	636
Db	416	AGCCAGGACCCAGAGAGATTAACCTGTTTCAATTGAAGATGCTAATTTTGGACGACAA	475
OY	637	TGAACATCAGTCTAAGTAGACGTCCAATGACCAAGACATGTACAAAGACCCGCGCA	696
Db	476	TATCTTATCAGCAGCAGCAGCTCATTTCTTCTGACATCTATGAGGCTCAACCAATTG	535
OY	697	TTTTCATATGGGGTTTATTTGCTGTAATCTCTTAACAAGATTTTGTAGAATACTTTGACC	756
Db	536	TGTTAAATGAACCTAAGTGCACAAAGGCCCTAATGAAATTTTCAAAAATTCGCGAG	595
OY	757	GTCACCATCTCTCATATGTCGACGTACTTTGGAAGTGCAAAGGCTTTTATGACAGTATC	816
Db	596	AAGACCCCTCATTAATTTGTGGCAGATTTTGGCAGTGCACACTGCCATAGCTCATATTC	655
OY	817	CGGGGATTAATGGGAACCGATGAA-----ATGAGACTATTTGCCTTGCACCTCA	867
Db	656	CAGTTCACCATGGGTGATTAATAGTAGAATCCCAATTAAGATTGACCTTTATGATGTAC	715
OY	868	GGAACCAAAATGGTACATCCAGCAGCAAACTTTCOCGAAAGCGTGGTATTTAGTTG	927
Db	716	GCAGAGAACCATGTCATCCAAAGAGCTGCATCTCTTAAGAAACATGCTTATTCGTGGT	775
OY	928	ACGTCAATGCGACATGAAGAAAGCACTCCGCTCACTATGCGCAAGAAAGATCATCA	987
Db	776	ATGAGATGGAATGTTTAGTGGATATGACCTTAACATGATCCGAACATCTGCTCCGAA	835
OY	988	TTTTGGATACACTTGGGATGATGACTTCTTCACATATATGCTTATATGAGAGCTTC	1047
Db	836	TGTTAGAAACCTCTCAGATGATGATTTGTGAATGTAAGTCTTATTAAGCAATGCTC	895
OY	1048	ACATATGGAACCTTGCTCGATGAACTTTGTCGAAGCCGACAGCAACAAAGAGC	1107
Db	896	AGGATGTAAAGCTGTTTTCAGCAC-----TTGTCGAAGCAAAATGTAGAAATTAAGAAAG	949
OY	1108	ACTTCAAGGAGCATCTGCAACAACCTTTTCGCCAAAGGAATTTGGAATGTTTCATTTACCTC	1167

Query Match	3.5%;	Score 130.6;	DB 9;	Length 3190;
Best Local Similarity	46.4%;	Pred. No. 3.4e-26;		
Matches 673;	Conservative 0;	Mismatches 739;	Indels 39;	Gaps 6

QY 346 AGAATATCAAGAGTATGAGAAAGACGTTGCCATAGAAAGAAATTGATGGCCCAACTGG 405
 Db 176 ATATTATGAGAAATATCAAGATTTGTATACTGTGAAACCAATTAATGACAGCCAGCTGG 235
 QY 406 TAAAGAGCTGGCAAGACATGAGAGATGTTTCACAGAACTCTGAGCCCTGACGGC 465
 Db 236 TAGAAATTTGACGCCAGGATTTGAGAAACCTTCGAGCAACGATCTTAACCCCTGGGGA 295
 QY 466 GTCTG-----GTGGAGCTGCAGAGAGACACCTGAAACATGAAATTTGATGAG 516
 Db 296 GCCCTGGCATTTGAGAGCGGAGAAAGTTCAAGCAGCTCACACAGAGAGAGATTTTGCA 355
 QY 517 ACTTACAGTATGAATTAATCTGCTGCTGATTAATGAAGGAGACAAAGCCGGAATT 576
 Db 356 GCATGAAATTTGCTCTACATGCAAAAGGATGATCTGATCCGAGAAATAATACAGTG 415
 QY 577 TTTTGGAGCTGGGAAAGAAATTCATCTTAGCCCAATGACCAATTTAATTAATTTGCC 636
 Db 416 AGCCAGGACCCAGAGATTAACCTGTTTCATTTGAAGATGCTAAATTTTGGACGACAA 475
 QY 637 TGAACATCAGTCTAAGTGTAGAGTCCAGTACCAAGCAATGTATACAAAGACCCCTGCA 696
 Db 476 TATCTTATCAGCAGCAGCAGCTCATATTCCTACTGACATCTATGAGGCTCAACAATTG 535
 QY 697 TTGTCATGAGGCTTATTTGCTGTAATCTCTAAACAAAGTTTGTAGATACTTTGACC 756
 Db 536 TGTAAATGAATCACTGAGCAAGTGCCTTAGATGAATGAATTTCAAAAGATGGCAGG 595
 QY 757 GTGACCATCTCATATGTCAGTACTTTGGAAGTGCMAAGGCTTTTATAGCAGTATC 816
 Db 596 AAGACCTTATTTATTTGTGTGGAGTTTGTGGAGTGCCTGCTGCTGATGATTTATC 655
 QY 817 CGGGGATTAATGGGAACGATGAGA-----ATGGAGTATTCCTGCTGACGCA 867
 Db 656 CAGCTTCACCATGGTTGATTAATGATGAACTCAAAATTAAGATTGACCTTTATGATGTAC 715
 QY 868 GGAACCGAAATGATGATCATCAGCAGCAACTCTCCGAAAGACGTGCTATTTAGTTG 927
 Db 716 GCAGAGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 775
 QY 928 AGCTGAGTGCACATGAAAGGACTCCGTGCTGATGCTGAGGAAACAACTCTATCCA 987
 Db 776 ATGTGAGTGAAGTGTAGTGAATGACACTTAACATGATCCGACATCTGCTCCGAAA 835
 QY 988 TTTTGGATACACTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1047
 Db 836 TGTTAAGAAACCTCTCAGATGATGATGATGATGATGATGATGATGATGATGATG 895
 QY 1048 ACTATGTGAACCTTGCCTGAATGAACCTTGTGCAAGCCGACAGGACAAACAAAGAGC 1107
 Db 896 AGGATGTAGCTGTGTTTCAGCACCC-----TTGTCAGAGCAATGTAAGAAATAAAAAG 949
 QY 1108 ACTTCAGGAGCATCTGAGCAAACTTTTGCCCAAGGAATGGAATGTTGATATAGCTC 1167
 Db 950 TGTGTAAGAACCGGCTGAATTAATATACAGCCAAAGAAATTACAGATTTAAGAAAGGCT 1009
 QY 1168 TGAATGAGCCCTTCAACATTTCTGATGATTTCAACACACAGGCAAGGAAGTATCTGCA 1227
 Db 1010 TTAGTTTTCCTTTGAAACACCTGCTTAATTAATATGTTTCCAGAGCA-----AACTGCA 1063
 QY 1228 GTACAGCCATCATCTCATTAATGATGAGGCGGTGACACCTATGATACAAATCTTTCAA 1287
 Db 1064 ATTAACATTTATTTATGCTATTTACAGGATGAGAGAAAGAGAGCCAGAGATATTTTACA 1123
 QY 1288 AATACAAATGGCCAGATGCAAAAGTTTCGATCTTTCATACCTCATTTGAGAGAGGCTG 1347
 Db 1124 AATACAAAT---AAAGATAAAAGATAGCTGATTTTCAGTTTGTCAACACAAATT 1180
 QY 1348 CATTTCAGACAAATCTAAAGTGGATGCTGTGCCAAAGAAAGATTTTACCAGATCT 1407
 Db 1181 ATGAGAGAGAGACTATTCAGTGTGATGCTGTGMAAACAAAGTTATTTATGAAATTC 1240
 QY 1408 CCAGCTTGCTGATGTGAGAGAAATGTCATGAAATACCTTCAGCTGCTTACCGGCCCA 1467

Db 1241 CTTCATTTGGTGCATATAGATCAATACATCTGAGAAATTTTGGATGTTTGGAGAGACCA 1300
 QY 1468 AAGTCAT-----CGACGAGAGCATGATGTGTGTGAGCCGGAAGCTTATGAGAGCA 1521
 Db 1301 TGGTTTTCAGAGAGACAAAGCTTAAGCAAGTCAATGAGACAAATGTGTACTGTGATCAT 1360
 QY 1522 CTCGATGATGATCAGAGCCCGCTGCTGATGACACTGTAGCCATGCTGTGTAGTA 1581
 Db 1361 TGGACTTGGAGCTTGTATTAATGAACTCTTCGGTCTTCAACATTAACGGCCAAATTG 1420
 QY 1582 AGCAGAACGAACCGATGCAAGGCGATTTCTGAGAGTGTGGCAAGATGTGCCAG 1641
 Db 1421 AAATTAAGCAAACTTAAGAACAGCTGATTTTGGTGTGATGAGAGTATGTGCTT 1480
 QY 1642 TGAAGAACTTCTGAGAGACCATCCCAAAATCAAGTTAGGATTCACGTTATGCTTTG 1701
 Db 1481 TGAAGATATTAAGAAAGCTGACACAGCTTTTACATGCTGCCCCAATGGGATTAATTTG 1540
 QY 1702 CAATCAAAATTAATGATATATCTGACGATCCGGAACAGCTGCTGTAGCAAGAG 1761
 Db 1541 CAATCGATCCTTAATGATGATTTTATTAATCAATCCAAATCTTCAACCAAGACCCAAAT 1600
 QY 1762 GAAAAAAGCA 1772
 Db 1601 CTCAGAGGCCA 1611

Search completed: Apr 11 28, 2003, 03:58:44
 Job time : 429 secs

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: April 27, 2003, 21:24:01 ; Search time 201 Seconds

(without alignments)
5752.096 Million cell updates/sec

Title: US-09-787-657-3

Perfect score: 3770

Sequence: 1 lactatagggcgccgca.....aaaaaaaaaaaaaaaa 3770

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
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4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	214	5.7	5463	4	US-09-470-443-1
2	214	5.7	5482	4	US-09-470-443-3
3	206.4	5.5	5279	4	US-09-470-443-5
4	130.6	3.5	3566	2	US-07-745-206A-24
5	130.6	3.5	3566	2	US-08-311-363-24
6	130.6	3.5	3579	2	US-08-455-543A-36
7	130.6	3.5	3579	2	US-08-193-078B-25
8	130.6	3.5	3579	2	US-08-223-305C-36
9	130.6	3.5	3579	3	US-08-949-386-32
10	130.6	3.5	3579	3	US-08-450-562-32
11	130.6	3.5	3579	4	US-08-984-709A-32
12	130.6	3.5	3579	4	US-08-450-272-32
13	130.6	3.5	3600	1	US-08-455-543A-11
14	130.6	3.5	3600	1	US-08-455-543A-33
15	130.6	3.5	3600	2	US-08-193-078B-11
16	130.6	3.5	3600	2	US-08-223-305C-11
17	130.6	3.5	3600	2	US-08-223-305C-33
18	130.6	3.5	3600	2	US-08-149-097D-11
19	130.6	3.5	3600	3	US-08-949-386-11
20	130.6	3.5	3600	3	US-08-450-562-11
21	130.6	3.5	3600	4	US-08-984-709A-11
22	130.6	3.5	3600	4	US-08-450-272-11
23	130.2	3.5	3564	1	US-08-455-543A-35
24	130.2	3.5	3564	2	US-08-193-078B-24
25	130.2	3.5	3564	2	US-08-223-305C-35
26	130.2	3.5	3564	2	US-08-949-386-31
27	130.2	3.5	3564	3	US-08-450-562-31

28	130.2	3.5	3564	4	US-08-984-709A-31	Sequence 31, Appl
29	130.2	3.5	3564	1	US-08-450-272-31	Sequence 31, Appl
30	130.2	3.5	3564	1	US-08-455-543A-34	Sequence 34, Appl
31	130.2	3.5	3585	2	US-08-193-078B-23	Sequence 23, Appl
32	130.2	3.5	3585	2	US-08-223-305C-34	Sequence 34, Appl
33	130.2	3.5	3585	3	US-08-949-386-30	Sequence 30, Appl
34	130.2	3.5	3585	3	US-08-450-562-30	Sequence 30, Appl
35	130.2	3.5	3585	4	US-08-984-709A-30	Sequence 30, Appl
36	130.2	3.5	3585	4	US-08-450-272-30	Sequence 30, Appl
37	130.2	3.5	3636	2	US-08-455-543A-32	Sequence 32, Appl
38	130.2	3.5	3636	2	US-08-193-078B-22	Sequence 22, Appl
39	130.2	3.5	3636	2	US-08-223-305C-32	Sequence 32, Appl
40	130.2	3.5	3636	3	US-08-949-386-29	Sequence 29, Appl
41	130.2	3.5	3636	3	US-08-450-562-29	Sequence 29, Appl
42	130.2	3.5	3636	4	US-08-984-709A-29	Sequence 29, Appl
43	130.2	3.5	3636	4	US-08-450-272-29	Sequence 29, Appl
44	130.2	3.5	3657	1	US-08-455-543A-20	Sequence 20, Appl
45	130.2	3.5	3657	2	US-08-223-305C-20	Sequence 20, Appl

ALIGNMENTS

```
RESULT 1
US-09-470-443-1
; Sequence 1, Application US/09470443
; Patent No. 6441156
; GENERAL INFORMATION:
; APPLICANT: Lerman, Michael I.
; APPLICANT: Minna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Boming
; APPLICANT: Du, Fuh-Mei
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
; FILE REFERENCE: NIH-05043
; CURRENT APPLICATION NUMBER: US/09/470,443
; EARLIER FILING DATE: 1999-12-22
; EARLIER APPLICATION NUMBER: 60/114,359
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 5463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (162)..(3599)
US-09-470-443-1
Query Match 5.7%; Score 214; DB 4; Length 5463;
Best Local Similarity 47.3%; Pred. No. 8e-42;
Matches 845; Conservative 0; Mismatches 900; Indels 41; Gaps 5;
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61 GGGCTGCGCCACCGCGCTCCGCGACGCTCCCGCGCGCTTCGTGCGCGCGAC 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
165 GGGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 224
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
225 TGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 284
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
181 GGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
285 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 344
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
241 GGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
345 TACACCTTC--CCCGACGACGACGATGACGACTGGGCGCGCGCGCGCGCGAGG 402
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
301 TAAATTCATTGCTCTTAAGTACTCGGTTCCCGACCTTCGCAAAAGAAATACAAAGT 360
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Db 403 TCGACGGGTGATGGGGATTTTGGAGCGCTCCAGACAGTCCGTGAGATTTTCAAGAGCA 462
Qy 361 ATGAGAAAGACGTTGCCCTAAGAAATTTGATGGCTTCAACTGGTAAAGAGCTGGCAA 420
Db 463 ACCGAAACCTGTTGAGGTACAGGAATGAGCCCTCAGAAATGTTGTGAGAGGTGGCAG 522
Qy 421 AGAATATGAGAGATGTTTCAAGAAAGTGTGAGCGCGTGTAGCGCTGTGTGAGAGCTG 480
Db 523 GGGACATTTGAGAGCTTCTGACAGAGAGTGTGAGCGCTGTAAAGAGACTGTGATGCTG 582
Qy 481 CAGAGAGACGACACCTGAAATTTGATGAGACTTACATGATGAAATCTT----- 535
Db 583 CAGAGAACTTCCAGAAAGACACCGCTGGCAGGACATCAAGAGAGAGAACATCGCT 642
Qy 536 -----CAATGCTGCTGATTAATGAAAGGACAAAGCGGAAT 576
Db 643 ACTATGACGCCAAGCTGAGCGCTGAGCTGACGACCTGAGAGATGTGAAAGGG 702
Qy 577 TTTTGGAGCTGGGAAAGAAATTCATCTTAGCCCAATGACCATTTTAATTAATTTGCTG 636
Db 703 GGTCTAAGCGCAGACACCTTAAGCTGAGCTTATCGAGAGACCAACTTCAAGAAAG 762
Qy 637 TGAACATCACTTAAGTGAAGTCCAAAGTACCAAGACATGTACAAAGAACCCCTGCA 696
Db 763 TCAACTATTCATACGGGGCTGTACAGATCCCTACGGACATCTCAAAAGCTCCACTGCA 822
Qy 697 TTTTCATGGGGTTTATGGTGTGAATCTCTAAACAAAGTTTTTGTAGATTAATTTGACC 756
Db 823 TCTCTAATGAGCTCAACTGACAGAGGCCCTGTGAGATGTTCATGTGAAACCGCAGAC 882
Qy 757 GTGACCATCTCTCATATGTGACAGTCTTGGAAAGTGTGAAAGGGCTTTTATGACAGATC 816
Db 883 AAGACCCCACTGCTGTGTGACAGTCTTGGCAGCGCAGAGAGTACTGTCTACTAC 942
Qy 817 CGGGATTTAATGGAAGCAGATGAGAAATGAGATTTGCCCTTGCATGCGCAACCGAA 876
Db 943 CGGCCACCCCTGGCAGGCCCAAGAAATGACCTGTACGATGTCCAGAGG---GAC 999
Qy 877 AATGATATCCAGGAGCAACTTCCGAAAGACGCTGATTTTATGATGAGCTGAGT 936
Db 1000 CCTGTATATCCAGGGGGCTCTCACCACCAAGACATGTGCATCATGTGATGTGATG 1059
Qy 937 GCAGCATGAAGGACTCCGCTGCTGACTATGCGAAGCAACAGCTCATCATTTTGGATA 996
Db 1060 GCAGTGTGAGCGGCTGACCTTAAGCTGATGAGACATCTGTCTCGAGATCTGGACA 1119
Qy 997 CACTTGGGATGATGACTTCTTCAACATATTGCTTATATGAGAGCTTCACTATGTG 1056
Db 1120 CGCTGTGATGATGACTATGTGAATGTGGCTCGTTCAACGAGAAAGGACACGCTGT 1179
Qy 1057 AACCTGGCTGAATGAACTTTGTGTGACAGCGCAGCAACAAAGAGCAGCTTGAAGG 1116
Db 1180 CATGCTTCAACACC-----TGTGTGAGGCCAATGTGGCAACAAAGAGTGTCAAG 1233
Qy 1117 AGCATCTGCAAAACTTTTCCGCAAAAGTGAATGTGATATAGCTGTGAATGAGAG 1176
Db 1234 AAGCTGTGAGGCAATGTGTGGCAAGGCAACAGGCTACAAAGCGCGCTTTGAGATG 1293
Qy 1177 CCTTCAACATTTCTGAGTATTTCAACACAGCGGACAAAGAGATATCTCACTAGGCA 1236
Db 1294 CTTTGTAGCAGCTGCAAGAACTCCAAACATCACTCGGGCC-----AAGTCAACAGATGA 1347
Qy 1237 TCATGCTCATATGATGAGGGGTGGAGACCTATGATATCAATCTTTGCAAAATCAAT 1296
Db 1348 TCATATGTTTCAAGGATGTGTGAGAGCCGCTGAGAGCTTTTGTGAGAGTCAAT 1407
Qy 1297 GGGCAGATGAAAGGTGTGCACTTACATACCATATTGAGAGAGAGAGCTGTGGCAG 1356
Db 1408 GGGCAACCGAGAGGTGGCGCTGTACTTCTCCGTGGGAGAGATTAATGACGCTCA 1467
Qy 1357 ACAATTAAGTGAATGAGCTGTGCAACAAAGATTTTATCCAGATCTCAGCTTGG 1416

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Db 1468 CACGCTCAGTGCATGCGCTGTGTGCAACAAAGCTACTATTTTGTAGATCCCTTCATCG 1527
Qy 1417 CTGATGTCCAGAGATGTCATGAAATCTTACGCTTACGCGGCCCAAGTCATCG 1476
Db 1528 GAGCATCCGATCAACACAGAGAAATATGATGTGTGTGGCAGGCCATGTGTCTGG 1587
Qy 1477 ACCAGAGCATGATGTGTGTGACCCAGAGCTTACATTTGACAGCACTGTGATGATC 1536
Db 1588 CAGGCAAGAGAGCCAGAGGTTTCAGTGACCAAGTGTATGAGAGATGCACTGGAGCTG 1647
Qy 1537 AGGGCCCCGCTGATGACCACTGTAGCCATCCCTGTGTTTATGACAGAACCA 1596
Db 1648 GGTGTGTGTACAGGAGCCCTCCCTTTTCAACTGACACAGATGCGCTGGGAAA 1707
Qy 1597 GATGAGAGGATCTTCTGAGAGTGTGTGGACAGATGTGCCAGTGAAGAACTTCTGA 1656
Db 1708 AGAAGAACAGCTATCTGTGGCGTATGAGCATTTGACGTGTGTATGATCAATCAAGA 1767
Qy 1657 AGACCATCCCAATACAGTTAGGATTCAGGGTTATGCTTTGCAATCAAAATATG 1716
Db 1768 GGTGACCCCACTACACCTGTGAGCCCAAGGCTATGTGTGTGCAATGTGACCTGAAG 1827
Qy 1717 GRTATCTGAGGACCTCCGAACTCAGGCTGTGTACGAAGAAAGAAAGGAAAGGA 1776
Db 1828 GCTAGTGTGTGACACCCCAATCTCAAGCCCAAGACCAACCTTCCGGAGGCTGTGA 1887
Qy 1777 AACCTAATATGATGAGCTTGTGACCTCTGTGAGGTGAGTGGAGAA 1822
Db 1888 CTCTGAGCTTCTGTGATGGGAGCTAGAGATGAGAAAGAAAGA 1933

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RESULT 2
US-09-470-443-3
; Sequence 3, Application US/09470443
; Patent No. 6441156
; GENERAL INFORMATION:
; APPLICANT: Lerman, Michael I.
; APPLICANT: Milna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Boping
; APPLICANT: Duh, Fuh-Mei
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
; FILE REFERENCE: NIH-05043
; CURRENT APPLICATION NUMBER: US/09/470,443
; EARLIER FILING DATE: 1999-12-22
; EARLIER APPLICATION NUMBER: 60/114,359
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patencin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 5482
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (181)..(3618)
US-09-470-443-3

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Query Match 5.7%; Score 214; DB 4; Length 5482;
Best Local Similarity 47.3%; Pred. No. 8e-42;
Matches 845; Conservative 0; Mismatches 900; Indels 41; Gaps 5;
Qy 61 GGGCTGCGCCACCGCGCTGCGGACGCTCCCGCGCGCTCTGTGTCGCCCGCGCAC 120
Db 184 GCGGTGCGCGGTGGAACCTGCGGCGCTCTGCGCGCGCGCAAGCGACTGCGCGCCC 243
Qy 121 GGGCGCTGCGAGAGGCCAAGCATGCGCGGCGCGGCTGCGCGCGCGCGCGCGCGG 180
Db 244 TGGCCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 303
Qy 181 GGGCTGCGCGCTTCTGCTGCGCGCGCTTCTGTACGCGCGCGCTGCGGAGCGTGTG 240

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[illegible]

Db	1367	TCATGATGTTCCAGGGATGCTGCTGATGAGCACCGCCGTGCAGGACCTCTTGGAGAACTGACAAATT	1426
Qy	1297	GGCCAGATCGAAGAGTTCCGCGATCTTTCACATACCTTCATTTGAGACGAGAGGCTGCCTTGGCAG	1356
Db	1427	GGCCAAACCGAGCGCTCGCGGTGTACTTCTCCGAGGGGACACATTAACATATGACGTCA	1486
Qy	1357	ACATCTTAAAGTGATGCTGCGCTGTGCCCAACAAGGATTTTTTACCAGATCTCCACCTTGG	1416
Db	1487	CACCGCGTGCAGTGGATGGCCCTGTGCCCAACAAAGGCTACTATTTTGAGATCCCTTCACATCG	1546
Qy	1417	CTGATGTGCAGGAGAAATGTCATGGGAATACCTTCACGCGCTTAAAGCCGCCCAACATCATCG	1476
Db	1547	GAGCCATCCGCATTCACACACAGGAATATCTAGATGTGTTGGGACGCCCATGTGTGCTGG	1606
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Db	1607	CAGGACAGGAGGCCACAGCAGATGTCAGTGAACACGCTGATGAGAGATGCACATGGGACTCG	1666
Qy	1537	AGGGCCCCGTCCTGATGATGACCACTGTATGCCATGCTGTGTTAGTAAGCAGAAAGCAACCA	1596
Db	1667	GGTGTGTGTAAACAGGAGCCCTCCCTGTTTTCAACTGACACACAGGATGGCCCTGGGAAA	1726
Qy	1597	GATCGAAGGGCATTTCTCTGGGAGTGTGTGGCACACAGATGTCGCCAGTGAAGAAACTTCTGA	1656
Db	1727	AGAGAGAACCAAGCTGATCTCGGCGCTGTATGGGCACTGACGGCTCTCAATATCATCATAGA	1786
Qy	1657	AGACCATCCCAATATACAAATTAGGCAATACGGTATATGCGCTTGCATCATCAATCAATATG	1716
Db	1787	GGCTGACCCCACTACACGCTTGGAGCCCAACGGCTATGTGTTGGCATTTGACTGGAAC	1846
Qy	1717	GRTATATCTCGACGCAATCCGGAACTCAGGCTGCTGTACGAAGAAGAAAAAGCGAAGA	1776
Db	1847	GCTACCTGTGGTCGACACCCCAATCTCAAGGCCCAAGACCACTTCCGGAGCGCTGGA	1906
Qy	1777	AACCTACTATATGATGAGCTTGCCTCTCTAGGTGGAGTGGGAAGA	1822
Db	1907	CTGTGAGTCTCTGATGCGGAGCTAGAGGATAGAAACAAGCAAGA	1952

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RESULT 3
US-09-470-443-5
: Sequence 5, Application US/09470443
: Patent No. 6441156
: GENERAL INFORMATION:
: APPLICANT: Lerman, Michael I.
: APPLICANT: Minna, John D.
: APPLICANT: Latif, Farida
: APPLICANT: Wei, Ming-Hui
: APPLICANT: Sekido, Yoshitaka
: APPLICANT: Gao, Boning
: APPLICANT: Duh, Fun-Wei
: TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
: FILE REFERENCE: NIH-05043
: CURRENT APPLICATION NUMBER: US/09/470,443
: CURRENT FILING DATE: 1999-12-22
: EARLIER APPLICATION NUMBER: 60/7114,359
: EARLIER FILING DATE: 1998-12-30
: NUMBER OF SEQ ID NOS: 114
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 5279
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (185)..(3415)
: US-09-470-443-5

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Query Match	5.58;	Score 206.4;	DB 4;	Length 5279;
Best Local Similarity	47.9%;	Pred. No. 5.3e-40;		
Matches 757;	Conservative 0;	Mismatches 786;	Indels 39;	Gaps 4
0y	265	TGGTGAACCTCTGGGGCCCTTTTGGTGGGGAATAAATTCATTTGCTGCTAAGTACT	324	

STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..3273
 US-07-745-206A-24

Query Match 3.5%; Score 130.6; DB 1; Length 3566;
 Best Local Similarity 46.4%; Pred. No. 8e-22;
 Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

346 AGAATACAAAGATGTGAGAAAGAGCGTTCCATGAGAGAAATGAGGCTCCCAACTG 405
 176 AATATTAGAGAAATATCAGATTGTGTATCTGTGGAAACCAATATATGACCCGACCTGG 235
 406 TAAAGAGCTGGCAAGAGATGAGATGTTTCCAGAAAGTGTGA 3GCCGTGAGGC 465
 236 TAGAATTGCAAGCCAGGATTTTGGAAACTTCTGAGCAACAGATCTTAAGCCCTGGTGA 295
 466 GTCTG-----GTGAGGCTGCAAGAGAGCAACACCTGAAACATGANTTTGATGCA 516
 296 GCGTCGCAATGAGAGGGAGAAAGTTCAAGCAAGCTCACAGTGGAGAGAGATTTTGCAA 355
 517 ACTTACAGTATGATCTCAATGCTGTGCTGATTAAGTAAAGGACAAAGAGCGGGAAT 576
 356 GCAATGAGATTGTCTTCAATGCAAAAGATGATCTCGATCCTGGAATAATGACAGT 415
 577 TTTTGGAGCTGGGAAAGATTCATCTTACCCCAATBACCATTTTAA 1PAATTTGCTG 636
 416 ACCGAGGAGCCAGAGAGATTAACCTGTTTCAATGAAAGATCTAATTTTGGACAGCAA 475
 637 TGAACATGAGTCAAGTCAAGTCAAGTCAAGCAAGCAAGTATGACAAAGAGACCTGCAA 696
 476 TATCTTATCAGACGACGAGTCAATCTTCTGACATCTATGAGGGCTCAACATTTG 535
 697 TTGTCAATGGGCTTTATTTGCTGTAATCTTAACAAAGTTTGTAGAACTTTGACC 756
 536 TGTTAATGAACTCAACGTGACAGTGCCTTATGATGAATTTTCAAAAAGTATGCGGAG 595
 757 GTGACCCATCTCTCATATGCGAGTACTTTGGAAGTGAAGGAGGCTTTT 1PAGGAGTATC 816
 596 AAGACCTTCTATTTATTTGGGAGGTTTGGCAGTGCCTGAGCTGATCTATTTATC 655
 817 CGGGATTAAATGGAGACAGATGAGA-----ATGAGTCAATTTGCTTCACTGCA 867
 656 CAGCTTCAACATGGGTGTATATAGTACACCAATTAAGATTGACCTTTATGATGAC 715
 868 GGAACCGAAATGTGACATCCAGCAGCAACTTCCGAAAGAGCGTGT 3ATTTTATGTTG 927
 716 GCAGAGACCATGCTACATCCAAAGAGCTGCATCTCTTAAGACATGCT 1ATTTGTTGG 775
 928 AGTCAGTGGGAGCATGGAAGGACTCCGCTGACATATCGCGAGAGAAACAGCTATCA 987
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 988 TTTTGGATACATTTGGGATGATCTTCAACATATTTGCTTATATA 1TGAGAGCTTC 1047
 836 TGTAGAAACCTCTCAATATATGATTTTCGTAATGATGATCTTATTA 3CAGAAATGCTC 895
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 1108 ACTTCAGGAGCATCTGCAAAACCTTTTCGCAAGAGAAATTTGATGAT 1T3GATATAGCTC 1167
 950 TGTGGAAGAGCGGTGATATATACACAGCAAGGAATTAACATTA 1FAAGAGGCT 1009
 1168 TGAATGAGGCTTCAACATTTGAGTATTCACACACAGGAGCAAGAGATATCTGCA 1227
 1010 TTAGTTTGTGTTGAACAGTGTGCTTATTAATGTTTCCAGAGCA-----AACTGCA 1063
 1228 GTCAAGGACATATGCTCATTAACATGAGGCGGTGACACCTATGATAC 1AATCTTTGCAA 1287

1064 ATAGATTTATTTATGCTATTTACAGGATGAGAGAGAGAGAGAGAGAGAGAGATTTTAA 1123
 1288 AATACATTTGGCAGATCGAAGGCTTGCATCTTCAATATACCATGAGAGAGAGCG 1347
 1124 AATACAT---AAAGATTAAGAGTACGTATTCAGTTTTCAGTTTTCAGTTTTCAGTTT 1180
 1348 CGTTTGCAGCAATCTAAGTGTGATGCTTGTGCAACAAAGATTTTACCAGATCT 1407
 1181 ATGAGAGAGAGACTTATTCAGTGTGATGCTTGTGCAACAAAGATTTATTTAAGAAATTC 1240
 1408 CCACTTGGCTGATGTCAGAGAGATGATGATATACCTTACGTGCTTACGCGGCCA 1467
 1241 CTTCATTTGTGCAATTAAGATCAATCAAGATATTTGGATGTTTGGAGAGACCA 1300
 1468 AGTCAAT-----CGACGAGAGCATGATGCTGTGAGAGAGAGAGAGAGAGAGAGAG 1521
 1301 TGGTTTACAGAGAGCAAAAGCTTAACCAAGTCCAAATGAGCAAAATGTTACTGTGATGCA 1360
 1522 CTCTGACTGATGATCAGGCGCCGCTGATGACCACTGATGACCATGCTGCTTTAGTA 1581
 1361 TGAAGTGGGACTTGTATCTATCTGGAACCTTCCGCTTCAACATTAACCGGCAATTTG 1420
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 1421 AAATTAAGCAAACTTAAGAAACACAGCTGATCTTGTGTGATGAGAGATGATGCTTT 1480
 1642 TGAAGAACTTCTGAAGACATCTCCCAATACAGATGATGAGATGATGATGATGATGAT 1701
 1481 TGAAGATATTTAAAGACATGACACCAAGTGTTAACATGCTGCCCCCAATGATATTTG 1540
 1702 CAATCAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1761
 1541 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1600
 1762 GAAAAAGGA 1772
 1601 CTCAGAGCCA 1611

RESULT 5
 US-08-311-363-24
 ; Sequence 24, Application US/08311363
 ; Patent No. 5876958
 ; GENERAL INFORMATION:
 ; APPLICANT: Harpold, Michael
 ; APPLICANT: Ellis, Steven
 ; APPLICANT: Williams, Mark
 ; APPLICANT: Feldman, Daniel
 ; APPLICANT: McCue, Ann
 ; APPLICANT: Brenner, Robert
 ; TITLE OF INVENTION: Human Calcium Channel Compositions and
 ; TITLE OF INVENTION: Methods
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/311.363
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/745.206
 ; FILING DATE: 15-AUG-1991
 ; ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 6362-51506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619)238-0999
 TELEFAX: (619)238-0062
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3566 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..3273
 US-08-311-363-24

Query Match 3.5% Score 130.6; DB 2; Length 3566;
 Best Local Similarity 46.4%; Pred. No. 8e-22;
 Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

QY 346 AGAATATCAAGAGTATGAGAAAGACCTGCCATAGAGAAATTTGATGCGCTCCAACTGG 405
 DB 176 ATATTTATGAAATATCAAGATTTTATCTGTGGAACCAATTAATGACGCGCACTGG 235
 QY 406 TAAAGAGCTGGCAAGAACATGAGAGATGTTTACAGAAAGTCTGAGCGCCCTCAGCC 465
 DB 236 TACAAATTTGACGACGAGATATGAGAACTTTGACCAACAGATCTAAAGCCCTGCTGA 295
 QY 466 GTTG-----GTGAGCGCTGCGAGAACACACACCTGAAACATATTTGATGACAG 516
 DB 296 GCGTGGCATTTGGAAGGAGAAAGTTCAAGACCTCACCAGGAGAGAAAGATTTTGCAA 355
 QY 517 ACTTACAGATGATATCTTCAATGCTGCTGTGTAATTAATGAAGGAGCAAGAGCGGAATT 576
 DB 356 GCAATGAACTGTCTACTACAAATGCAAGAGATCTCGATCCCTGAGAAAAATGACAGTG 415
 QY 577 TTTTGGAGCTGGGAAGAAATTCATCTTAGCCCAATGACCTTTTAATTAATTTGCCG 636
 DB 416 AGCAGGAGCAGCAGAGATTAACCTGTTTCAATGAGATGCTAATTTTGGACGACAAA 475
 QY 637 TGAACATCACTTAAGTGAAGTCCAAAGCAAGCAATGTAACAAGAAAGACCTGCAA 696
 DB 476 TATCTTATGACGACGACGATGATCTGATGATGATGATGATGATGATGATGATG 535
 QY 697 TGTCAATGAGGTTTATGCTGCTGAATCTCTAACAAGATTTTGTAGATTAATCTTGACC 756
 DB 536 TGTAAATGAATCACTCAACAGTGCCTTAGATGAATGATTAACAAAGAAATCCGAGG 595
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 QY 817 CGGGATTAATGGAACAGATGAGA-----ATGAGTCAATGCTCTGCACTGCA 867
 DB 656 CAGCTTCAACATGGGTATATAGTAACTCAAAATTAAGATTAACCTTTATGATGAC 715
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 DB 716 GCAGAGACCAATGTAACAGAGAGTGCATCTTAAGACATGCTTATTTGAGTG 775
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 DB 836 TGTAGAGAAACCTCTCAATGATGATGATGATGATGATGATGATGATGATGATG 895
 QY 1048 ACTATGAGAACTTGGCTGAATGAACTTTGGTGAAGCCGACAGCAAGCAAGAGC 1107
 DB 896 AGCATGTAAGCTGTTTTCAGAC-----TTGTCCAAGCAAAATGTAAGAAATAAAG 949

QY 1108 ACTTCAGGAGACATCTGACAACTTTTCCGCAAGAAATTTGATGATGATGATGATGATG 1167
 DB 950 TGTGAAAGACGCGGTGAATATATACAGCCAAAGAAATTAAGATTTAAGAGGCT 1009
 QY 1168 TGAATGAGCGCTTCAACATTTGTAGTATTTCAACACACAGCGGCAAGAAATTTGCA 1227
 DB 1010 TTAGTTTGTCTTTGAACAGCTGCTTAATTAATGTTTCCAGAGCA-----AACTGCA 1063
 QY 1228 GTACGCCATCATCTGATTAATGATGATGATGATGATGATGATGATGATGATGATG 1287
 DB 1064 ATAGATTAATTAATCTTATCAAGATGATGATGATGATGATGATGATGATGATGATG 1123
 QY 1288 AATTAATTTGGCAGATGGAAGGTTGCACTTTCACATCTCATTTGAGAGAGCGCTG 1347
 DB 1124 AATCAAT-----AAAGATTAAGAAAGTACGTGATTCAGTTTTCAGTTGCAACACAT 1180
 QY 1348 CGTTTGCAGCAATCTTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1407
 DB 1181 ATGAGAGAGACCTTATTCAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1240
 QY 1408 CCACTTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1467
 DB 1241 CTTCATTTGCTGATTAAGATTAATCAATTAATCAATTAATTAATTAATTAATTAAT 1300
 QY 1468 AACTCAT-----CGACCAAGACATGATGATGATGATGATGATGATGATGATGATG 1521
 DB 1301 TGGTTTATGAGAGAGCAAAAGTAAAGCAATGCAATGCAATGCAATGCAATGCAAT 1360
 QY 1522 CTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1581
 DB 1361 TGAAGTGGAGCTTGTCAATTAATGATGATGATGATGATGATGATGATGATGATGATG 1420
 QY 1582 AGCAGACGAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1641
 DB 1421 AAATTAAGCAAACTTAAGAAACACACTGATTTTGTGTGATGAGATGATGATGATG 1480
 QY 1642 TGAAGACTTCTGAAGACCATCCCAAAATACAAAGTTAGATGATGATGATGATGATG 1701
 DB 1481 TGAAGATTAATTAAGACATGACACACGTTTAACTGATGATGATGATGATGATGATG 1540
 QY 1702 CAATCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1761
 DB 1541 CAATGATCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1600
 QY 1762 GAAAAAGCA 1772
 DB 1601 CTCAGAGGCA 1611

RESULT 6
 US-08-455-543A-36
 : Sequence 36, Application US/08455543A
 : Patent No. 5792846
 :
 : GENERAL INFORMATION:
 : APPLICANT: Harpold, Michael
 : APPLICANT: Ellis, Steven
 : APPLICANT: Williams, Mark
 : APPLICANT: Feldman, Daniel
 : APPLICANT: McCue, Ann
 : APPLICANT: Brenner, Robert
 : TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 : TITLE OF INVENTION: METHODS
 : NUMBER OF INVENTION: 57
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Brown, Martin, Haller & McClain
 : STREET: 1660 Union Street
 : CITY: San Diego
 : STATE: California
 : COUNTRY: USA
 : ZIP: 92101-2926
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/455,543A
 FILING DATE: May 31, 1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/223,305
 FILING DATE: April 4, 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/868,354
 FILING DATE: April 10, 1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/745,206
 FILING DATE: 15-AUG-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/620,250
 FILING DATE: 30-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/482,384
 FILING DATE: 20-FEB-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/603,751
 FILING DATE: 04-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US89/01408
 FILING DATE: 04-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/176,899
 FILING DATE: 04-APR-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L.
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 6362-52517
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619)238-0999
 TELEFAX: (619)238-0062
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3579 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: Genomic DNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 FEATURE:
 NAME/KEY: Coding Sequence
 LOCATION: 35...3289
 OTHER INFORMATION: Standard name "alpha2"
 NAME/KEY: 5'UTR
 LOCATION: 1...34
 OTHER INFORMATION:
 NAME/KEY: 3'UTR
 LOCATION: 3290...3579
 OTHER INFORMATION:
 US-08-455-543A-36

Query Match 3.5%; Score 130.6; DB 1; Length 3579;
 Best Local Similarity 46.4%; Pred. No. 8e-22;
 Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

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 Db 630 AAGACCTTCATTATTGTGACAGGTTTGGACAGTGCACAGTGCACAGTGCACAGTGCACAGT 689
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 Db 1044 TTAGTTTCTTTTGAACAGCTGCTTAATTAATATGTTTCCAGAGCA-----ACTGCA 1097
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Db 1635 CTCAGAGCCA 1645

RESULT 7
US-08-193-078B-25
Sequence 25, Application US/08193078B
Patent No. 5846757
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWN, MARTIN, HALLER & MCCLAIN
STREET: 1660 UNION STREET
CITY: SAN DIEGO
STATE: CA
COUNTRY: USA
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,078B
FILING DATE: 07-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/868,354
FILING DATE: 10-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seldman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-53607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 3579 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 35..3289
OTHER INFORMATION: /standard_name="Alpha-2e"

FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..34
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 3289..3579
US-08-193-078B-25

Query Match 3.5%; Score 130.6; DB 2; Length 3579;
Best Local Similarity 46.4%; Pred. No. 8e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

QY 346 AGAATATCAAAAGCTATGAGAAAGACCTTGGCATAGAAAGAAATGATGGCTCCCACTGG 405
Db 210 ATATTATGAGAAATATCAAGATTGTATACGTGGAACCAAAATATGACAGCCAGCTGG 269
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QY 466 GTCTG-----GTGAGAGCTGCAGAGAGAGACACCTGAAACATGATTTGATGACAG 516
Db 330 GCGTGGCATTTGGAAGCGGAGAAAGTTCAACAGCTCCAGTGAGAGAGATTTTGCAG 389
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Db 630 AAGACCTTCAATATTTGAGGAGGTTTGGCAGGCTGCTGAGCTGCTGATTTATTC 689
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Db 750 GCAGAAAGACATGTATCATCCAAAGAGCTGATCTCTAAGACATGCTTATTTGCTGG 809
QY 928 AGCTGAGTGGAGCATGGAAGAGACTCCGTGACATATGCGGAGCAAGCAAGCTTCATCA 987
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      APPLICATION NUMBER: US 07/745,206
      FILING DATE: 15-AUG-1991
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/620,250
      FILING DATE: 30-NOV-1990
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/482,384
      FILING DATE: 20-FEB-1990
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/603,751
      FILING DATE: 04-APR-1989
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: WO PCT/US89/01408
      FILING DATE: 04-APR-1989
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/176,899
      FILING DATE: 04-APR-1988
      ATTORNEY/AGENT INFORMATION:
      NAME: Seidman, Stephanie L.
      REGISTRATION NUMBER: 33,779
      REFERENCE/DOCKET NUMBER: 52516 (P519739)
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (619)238-0999
      TELEFAX: (619)238-0062
      INFORMATION FOR SEQ ID NO: 36:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 3579 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
      MOLECULE TYPE: Genomic DNA
      HYPOTHEetical: NO
      ANTI-SENSE: NO
      FRAGMENT TYPE: NO
      ORIGINAL SOURCE:
      FEATURE:
      NAME/KEY: Coding Sequence
      LOCATION: 35...3289
      OTHER INFORMATION: Standard name "alpha2e"
      NAME/KEY: 5'UTR
      LOCATION: 1...34
      OTHER INFORMATION:
      NAME/KEY: 3'UTR
      LOCATION: 3290...3579
      OTHER INFORMATION:
      ?
      ?
      ?
      US-08-223-305C-36
    Query Match          3.5%, Score 130.6; DB 2; Length 3579;
    Best Local Similarity 46.4%; Pred. No. 8e-22;
    Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps
    QY   346 AGAATACAAAGAGATGATGAGAAGACGTGGCATTGAGAAATTTATGCGCTCCCAACTGG 405
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    Db   210 ATATTATTGAACAATAATCAAGATTTTGTATCTGTGGAAACCAATTAATCACGCCAGCTGG 269
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Db 510 TATCTTATCAGCAGCAGCATCCATATTTCTACTGATCTATGAGGGCTCAACAAATTG 569
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Db 630 AAGACCTCTTATTTATTTGGAGGTTTGTGGACAGTGCACCTGACCTGATGATATATC 689
OY 817 CGGGGATTAATGGGAACCAAGATGAGA-----ATGAGTCATTTGCTTCGACTGCA 867
Db 690 CAGCTTCACCATGGGTGATTAATAGTAACCTCCAATTAAGATTAAGCTTATGATGATC 749
OY 868 GGAACCGAATGGTATCATCAGGACCACTTCTCCGAAAGAGCTGCTATTTTACTTG 927
Db 750 GCAGAGACCATGTTACATCCAAAGAGCTGCTCTCTAAAGACATCTTAATCTGCTGG 809
OY 928 AGCTCAGTGCACATGAAAGACCTCGTCTGACTATCGGAAAGCAAGCTCATCCA 987
Db 810 ATGTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 869
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Db 1044 TTAGTTTCTTTTGAACGCTGCTTAATTAATTAATTTTCCAGAGCA-----ACTGCA 1097
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Db 1158 AATTAATTTGGCCATGCAAGGTTCCGCTTCTCATATCTCATATCTTGGAGAGAGCTG 1214
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Db 1635 CTCAGAGACCA 1645

RESULT 9
US-08-949-386-32
Sequence 32, Application US/08949386
Patent No. 6090623
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: McCue, Ann
APPLICANT: Gillespie, Allison
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: US
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/949,386
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/290,012
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 08/149,097
FILING DATE: 5-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,536
FILING DATE: 11-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 519808
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 238-0999
TELEFAX: (619) 238-0062
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 3579 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 35..3289
OTHER INFORMATION: /standard_name="Alpha-2e"
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..34
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NAME/KEY: 3'UTR
LOCATION: 3289..3579
US-08-949-386-32

Query Match 3.5%; Score 130.6; DB 3; Length 3579;
Best Local Similarity 46.4%; Pred. No. 8e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;


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1  PRIOR APPLICATION DATA:
2  APPLICATION NUMBER: 08/223,305
3  FILING DATE: 4-APR-1994
4  PRIOR APPLICATION DATA:
5  APPLICATION NUMBER: 08/193,078
6  FILING DATE: 07-FEB-1994
7  PRIOR APPLICATION DATA:
8  APPLICATION NUMBER: 08/149,097
9  FILING DATE: 5-NOV-1993
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: 08/105,536
12 FILING DATE: 11-AUG-1993
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: 07/914,231
15 FILING DATE: 13-JULY-1992
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: 07/868,354
18 FILING DATE: 10-APR-1992
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: PCT/US92/06903
21 FILING DATE: 14-AUG-1992
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: 07/745,206
24 FILING DATE: 15-AUG-1991
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: 07/620,250
27 FILING DATE: 30-NOV-1990
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: 07/603,751
30 FILING DATE: 08-NOV-1990
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: 07/482,384
33 FILING DATE: 02-FEB-1990
34 PRIOR APPLICATION DATA:
35 APPLICATION NUMBER: PCT/US89/01408
36 FILING DATE: 04-APR-1989
37 PRIOR APPLICATION DATA:
38 APPLICATION NUMBER: 07/176,899
39 FILING DATE: 04-APR-1988
40 ATTORNEY/AGENT INFORMATION:
41 NAME: Seidman, Stephanie L.
42 REGISTRATION NUMBER: 33,779
43 REFERENCE/DOCKET NUMBER: 6362-519812
44 TELECOMMUNICATION INFORMATION:
45 TELEPHONE: (619) 238-0999
46 TELEFAX: (619) 238-0062
47 INFORMATION FOR SEQ ID NO: 32:
48 SEQUENCE CHARACTERISTICS:
49 LENGTH: 3579 base pairs
50 TYPE: nucleic acid
51 STRANDEDNESS: double
52 TOPOLOGY: linear
53 MOLECULE TYPE: DNA (genomic)
54 FEATURE:
55 NAME/KEY: CDS
56 LOCATION: 35..3289
57 OTHER INFORMATION: /standard_name="Alpha-2e"
58 FEATURE:
59 NAME/KEY: 5'UTR
60 LOCATION: 1..34
61 FEATURE:
62 NAME/KEY: 3'UTR
63 LOCATION: 3289..3579

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Query Match	3.5%	Score 130.6	DB 3	Length 3579
Best Local Similarity	46.4%	Pred. No. 8e-22		
Matches	673	Conservative	0	Mismatches 739
				Indels 39
				Gaps 6
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Db	1158	AATTCATTT-----AAGATTAATAAAGATGACGHTAGTACAGTTTTCACTGTGTCAACACAA	1214
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RESULT 12

US-08-450-272-32

Sequence 32, Application US/08450272

Patent No. 6387696

GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark

APPLICANT: McCue, Ann

APPLICANT: Gillespie, Allison

APPLICANT: Feldman, Daniel

APPLICANT: Brenner, Robert

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

METHODS

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESS: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: California

COUNTRY: US

ZIP: 92101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,272

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/404,950

FILING DATE: 13-MAR-1995

APPLICATION NUMBER: 08/336,257

FILING DATE: 7-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/314,083
FILING DATE: 28-SEPT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/311,363
FILING DATE: 23-SEPT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,012
FILING DATE: 11-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: 4-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/193,078
FILING DATE: 07-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/149,097
FILING DATE: 5-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,536
FILING DATE: 11-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/914,231
FILING DATE: 13-JULY-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: 10-APR-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06903
FILING DATE: 14-AUG-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/745,206
FILING DATE: 15-AUG-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-519812
TELEPHONE: (619) 238-0999
TELEFAX: (619) 238-0062
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 3579 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 35..3289
OTHER INFORMATION: /standard_name="Alpha-2e"
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..34
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 3289..3579
US-08-450-272-32

Query Match 3.58; Score 130.6; DB 4; Length 3579;
Best Local Similarity 46.4%; Pred. NO. 8e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;
346 AGAATACAAAGAGTATGAGAAACGTTGGCATGAGAAATGATGCGCTCCACTCG 405
210 ATATTATGAGAAATATCAACAGATTGTTACTGTGGAACCAATATATGACGCGAGCTGG 269


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APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 35..3310
OTHER INFORMATION: /standard_name= "Alpha-2"
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..34
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LOCATION: 3308..3600
US-08-455-543A-11

Query Match      3.5%; Score 130.6; DB 1: Length 3600;
Best Local Similarity 46.4%; Pred. No. 8e-22;
Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

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OY 577 TTTTGAGCTGGAAAGAGATTCATCTTAAGCCCAATGACATTTTAATTAATTTGGCTG 636
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DB 510 TATCTTATCAGACGACGACATGCTCATTTCTACTGACATCTATAGAGGCTCAACAATTTG 569
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DB 1098 ATAGATTTATTTATGCTATTCACGATGAGAGAGAGAGAGAGAGCCAGAGATTTTAACA 1157
OY 1288 AATACATTTGGCCAGATTCGAAGGTTGCGATCTTCACATCTCATGAGCGAGAGGCTG 1347
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DB 1575 CAATGATCTTAATGTTATGTTTATATACATCCAAATCTTACAGCAAAAGAACCCCAAT 1634
OY 1762 GAAAAAAGCGA 1772
DB 1635 CTCAGAGACCA 1645

RESULT 14
US-08-455-543A-33
Sequence 33 Application US/0845543A
Patent No. 5792846
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: Mccue, Ann
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1  APPLICANT: Brenner, Robert
2  TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
3  NUMBER OF INVENTION: METHODS
4  TITLE OF INVENTION: METHODS
5  NUMBER OF SEQUENCES: 57
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: Brown, Martin, Haller & McClain
8  STREET: 1660 Union Street
9  CITY: San Diego
10 STATE: California
11 COUNTRY: USA
12 ZIP: 92101-2926
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Diskette
16 COMPUTER: IBM Compatible
17 OPERATING SYSTEM: DOS
18 SOFTWARE: FASTSEQ Version 1.5
19
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/455,543A
22 FILING DATE: May 31, 1995
23
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: 08/223,305
26 FILING DATE: April 4, 1994
27
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: 07/868,354
30 FILING DATE: April 10, 1992
31
32 PRIOR APPLICATION DATA:
33 APPLICATION NUMBER: US 07/745,206
34 FILING DATE: 15-AUG-1991
35
36 PRIOR APPLICATION DATA:
37 APPLICATION NUMBER: US 07/620,250
38 FILING DATE: 30-NOV-1990
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40 PRIOR APPLICATION DATA:
41 APPLICATION NUMBER: US 07/482,384
42 FILING DATE: 20-FEB-1990
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44 PRIOR APPLICATION DATA:
45 APPLICATION NUMBER: US 07/603,751
46 FILING DATE: 04-APR-1989
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48 PRIOR APPLICATION DATA:
49 APPLICATION NUMBER: WO PCT/US89/01408
50 FILING DATE: 04-APR-1989
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52 PRIOR APPLICATION DATA:
53 APPLICATION NUMBER: US 07/176,899
54 FILING DATE: 04-APR-1988
55
56 ATTORNEY/AGENT INFORMATION:
57 NAME: Seidman, Stephanie L.
58 REGISTRATION NUMBER: 33,779
59 REFERENCE/DOCKET NUMBER: 6362-52517
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61 TELECOMMUNICATION INFORMATION:
62 TELEPHONE: (619)238-0999
63 TELEFAX: (619)238-0062
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65 INFORMATION FOR SEQ ID NO: 33:
66 SEQUENCE CHARACTERISTICS:
67 LENGTH: 3600 base pairs
68 TYPE: nucleic acid
69 STRANDEDNESS: double
70 TOPOLOGY: linear
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72 MOLECULE TYPE: DNA (genomic)
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74 FEATURE:
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76 LOCATION: 35..3310
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RESULT 15 US-08-193-078B-11

Sequence 11, Application US/08193078B
 Patent No. 5846757

GENERAL INFORMATION:

APPLICANT: Harpold, Michael
 APPLICANT: Ellis, Steven
 APPLICANT: Williams, Mark
 APPLICANT: Feldman, Daniel
 APPLICANT: McCue, Ann
 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWN, MARTIN, HALLER & MCCLAIN
 STREET: 1660 UNION STREET
 CITY: SAN DIEGO
 STATE: CA
 COUNTRY: USA
 ZIP: 92101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/193,078B
 FILING DATE: 07-FEB-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/868,354
 FILING DATE: 10-APR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/745,206
 FILING DATE: 15-AUG-1991

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INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:

LENGTH: 3600 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 35..3310
 OTHER INFORMATION: /standard_name="Alpha-2b"
 FEATURE:
 NAME/KEY: 5'UTR
 LOCATION: 1..34
 NAME/KEY: 3'UTR
 LOCATION: 3308..3600
 US-08-193-078B-11

Query Match

Best Local Similarity 46.48; Score 130.6; DB 2; Length 3600;
 Matches 673; Conservative 0; Mismatches 739; Indels 39; Gaps 6;

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Search completed: April 28, 2003, 01:20:19
 Job time : 224 secs

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